



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 125803

TO: Bridget Bunner
Location: REM/4C65/4C70
Art Unit: 1647
Wednesday, June 30, 2004

Case Serial Number: 10/069034

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Thank you for using STIC services.

STIC-Biotech/ChemLib

105803

From: Bunner, Bridget
Sent: Monday, June 28, 2004 3:24 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like request a sequence search for case 10/069,034:

1. the amino acid sequence of SEQ ID NO: 28
2. the nucleic acid sequence of SEQ ID NO: 65

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

Searcher: Arnold
Phone: 3-2532
Location: _____
Date Picked Up: 6/29/04
Date Completed: 6/30/04
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2004, 10:57:45 ; Search time 22 Seconds
(without alignments)
1074.759 Milli:cn cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265
Sequence: 1 MAWASRLGILLALLPFWGA.....PEIFVYGVYVWISSGLFYQS 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5a COMB.pap.*
2: /cgn2_6/prodata/2/iaa/5a COMB.pap.*
3: /cgn2_6/prodata/2/iaa/5a COMB.pap.*
4: /cgn2_6/prodata/2/iaa/5a COMB.pap.*
5: /cgn2_6/prodata/2/iaa/5a COMB.pap.*
6: /cgn2_6/prodata/2/iaa/5a COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	286	12.6	487	3	US-08-431-517F-4
2	283	12.5	487	1	US-08-030-644-2
3	283	12.5	487	1	US-08-013-831-2
4	283	12.5	487	1	US-08-072-063-2
5	283	12.5	487	1	US-08-212-132-2
6	283	12.5	487	1	US-08-414-924-2
7	283	12.5	487	1	US-08-311-611A-69
8	283	12.5	487	1	US-08-311-611A-146
9	283	12.5	487	1	US-08-173-968-2
10	283	12.5	487	1	US-08-232-521-2
11	283	12.5	487	1	US-08-372-783-69
12	283	12.5	487	1	US-08-372-783-146
13	283	12.5	487	1	US-08-372-105-69
14	283	12.5	487	1	US-08-372-105-146
15	283	12.5	487	1	US-08-415-158-2
16	283	12.5	487	1	US-08-064-693-2
17	283	12.5	487	1	US-08-391-112-2
18	283	12.5	487	1	US-08-306-473A-69
19	283	12.5	487	1	US-08-306-473A-146
20	283	12.5	487	1	US-08-430-417-2
21	283	12.5	487	1	US-08-557-287-2
22	283	12.5	487	1	US-08-470-366-2
23	283	12.5	487	1	US-08-261-660A-12
24	283	12.5	487	1	US-08-209-762-69
25	283	12.5	487	1	US-08-644-290-2
26	283	12.5	487	1	US-08-378-228-2
27	283	12.5	487	1	US-08-927-438-2

28 283 12.5 487 1 US-08-473-344-69 Sequence 69, Appli
29 283 12.5 487 1 US-08-274-303-2 Sequence 2, Appli
30 283 12.5 487 1 US-07-915-720D-13 Sequence 13, Appli
31 283 12.5 487 1 US-08-435-855-2 Sequence 2, Appli
32 283 12.5 487 2 US-08-466-822-2 Sequence 2, Appli
33 283 12.5 487 2 US-08-466-824-2 Sequence 2, Appli
34 283 12.5 487 2 US-08-621-803-265 Sequence 265, App
35 283 12.5 487 2 US-08-466-826-2 Sequence 2, Appli
36 283 12.5 487 2 US-08-704-504-2 Sequence 2, Appli
37 283 12.5 487 2 US-08-485-445A-69 Sequence 69, Appli
38 283 12.5 487 2 US-08-485-445A-146 Sequence 146, App
39 283 12.5 487 2 US-08-621-259A-252 Sequence 252, App
40 283 12.5 487 2 US-08-586-133-2 Sequence 2, Appli
41 283 12.5 487 2 US-09-063-432-2 Sequence 2, Appli
42 283 12.5 487 2 US-08-862-785A-2 Sequence 2, Appli
43 283 12.5 487 2 US-09-081-166-2 Sequence 2, Appli
44 283 12.5 487 2 US-09-203-159-2 Sequence 2, Appli
45 283 12.5 487 3 US-09-099-725-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-431-517F-4
; Sequence 4, Application US/08431517F
; Patent No. 6265187
; GENERAL INFORMATION:
; APPLICANT: Scott, Randal W
; APPLICANT: Marra, Marian N
; TITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS
; FILE REFERENCE: 1103/113070501
; CURRENT APPLICATION NUMBER: US/08/431,517F
; CURRENT FILING DATE: 1995-05-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 487
; TYPE: PRT
; ORGANISM: human
; OTHER INFORMATION: BPI cDNA and amio acid sequence (Figure 3)
US-08-431-517F-4

Query Match 12.6%; Score 286; DB 3; Length 487;
Best Local Similarity 22.4%; Pred. No. 3.2e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASSLGLALLPVGASTPTGTVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58
DB 15 WWS-LMWLVAIGTAVTAANNPGVVVRISQGLDYASQQTALQKELKRIKIDYDSFK 73
QY 59 -----WSGEALQPTIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106
DB 74 IKHLGKHGHSFYSDMIREFQLPSSQISVNPVGLKFSISNANIKISGKWAQKRFKLSMG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACLSGSHANEFGDSNSTSHA--LLVLVQ 162
DB 134 NFDLSIEGMSIGADLKLGSNPTSGKPTITCSSC---SSHINSVHVHISKVGMLIQLFH 190
QY 163 KHITKAVLSNKL---CLISNLVQG-VNVHLGLTGLNVPGPSQIRYSVMVPTVTSY 217
DB 191 KLESALRNKMSQVCKVNSVSSKLOQYFQTLPMWKIDSVAGINYGIVAPNTAET 250
QY 218 ISLEVNAVFLLLKPIILPTDTPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275
DB 251 LDVQMKGEFYSENH-----HNPPFPAPPWMEFAHDMVYVGLSDYFFNTAGLVQEG 305
QY 276 ALNLDITGQL--RSDNLTNTSALGLIIEVARQFPPEPMPVLKVLGATFVAMLHTNNA 333
DB 306 VLKMTLRDDMIKPKESKRITTKFPFGFLPEVAKKFN--MKIQIHVSASTPPLHSVQPT 362
QY 334 TLRLQPFVEV--LATASNSAFQSLFSLDVVNLRLQLSVSKVLQQTTSVLGQVQLTVAS 391

Db 363 GLTFYPAVDVQALAVLPNSLSASLFLIGHHTTGSMEVSAESNRLVGELK-LDRLLLELKH 421
QY 392 SNVGFIDTDVRLTGMVPEKPLDLHLNALLAMGIALPGVWMLHYVAPFIFFYEGYVVIS 451
Db 422 SNIGFFPVLLQDIMNYIVPILVPRVNEKLOKGFPLTPARVQVLYNMYVLPQHPHFLFEG 481
QY 452 SOLFYQ 457
Db 482 ADVYK 487

RESULT 2
US-08-030-644-2
; Sequence 2, Application US/08030644
; Patent No. 5348942
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G. II
; APPLICANT: Gazzano-Santoro, Helene
; APPLICANT: Parent, James Brian
; TITLE OF INVENTION: Therapeutic uses of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Products
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,644
; FILING DATE: 19930312
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 31229
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-030-644-2

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLALLLPYVGASTGCTGVVRLNKAALSYVSEIGKAELOAL-QVTVPHFLD--- 58
Db 15 WVS-LMVLVAGTAVTAANVGNVVRISQKGLDYASQQAALQKELKRIKIPDYSDSFK 73
QY 59 -----WSGALOPTRIRILNVH---VPRHLXP-IAGFGVRLAAANFTFKVRAPE 106
Db 74 IKHLCKGVSYFMSDIRFQLPSSQISMPVNTGLAFESINAIKISGKKAQKFLKWSG 133
QY 107 PLELTP-LVELADTRV-TQSSIRTPVVISACS-LFSGHANEFDCGNSNTSHA--LLVLVQ 162
Db 134 NFDLSIEGMSISADLKLSNPTSGKPTITCSC---SSHINSVHVHISKVKVGLIQLFH 190
QY 163 KHIAVLNKL-----CLISNLVQV-VNVHLGTL-GLAPVGPESQIRYSMSVPTVSDY 217
Db 191 KKIESALRNKMSQVCEKVTNSVSSKLQYFOTLPVMTKIDSVAGINYLVAAPPATTAET 250

QY 218 ISLEVNVLFLGKPIILPTDATPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275
Db 251 LDVQMKGEFYSNH-----HNPPFPAPPVWMEFPAADRVMVYLGSLDYFFNTAGLVYQEAG 305
QY 276 ALNLITGOL--RSDNLTNTSALGRLEPEVARQFPEPMFVVLKVRLGATPPVAMLHTNNA 333
Db 306 VLKMTLRDDMIPKESKRLTTKFFGTFLPEVAKKFPN--MKIQIHVSASTPPLSVQPT 362
QY 334 TLRQPFVEVLATA--SNSAFOSLSLSDVVMNRLQLSVSKVLOQTTSVLGDVQVLTVAS 391
Db 363 GLTFYPAVDVQAFVLPNLSLASLFLIGHHTTGSMEVSAESNRLVGELK-LDRLLLELKH 421
QY 392 SNVGFIDTDVRLTGMVPEKPLDLHLNALLAMGIALPGVWMLHYVAPFIFFYEGYVVIS 451
Db 422 SNIGFFPVLLQDIMNYIVPILVPRVNEKLOKGFPLTPARVQVLYNMYVLPQHPHFLFEG 481
QY 452 SOLFYQ 457
Db 482 ADVYK 487

RESULT 3
US-08-013-801-2
; Sequence 2, Application US/08013801
; Patent No. 5420019
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Horwitz, Arnold
; APPLICANT: Burke, David
; APPLICANT: Baltaian, Manik
; APPLICANT: Grinna, Lynn S
; TITLE OF INVENTION: Stable Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical
; TITLE OF INVENTION: Compositions Containing the Same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; CITY: Two First National Plaza
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,801
; FILING DATE: 02 FEB 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 27129/30911
; TELEPHONE: 312/346-5750
; TELEFAX: 312/346-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-013-801-2

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY	3	WASRLGILLALLLFPWGASTFGTVVRLNKAALSYVSEIGKAPLQCAL-QVTVPHFLD---	58
Db	15	KVS-LMVLAIGTAVTAANPGVVVRIISGKGLDVASQQGTAALQKELKRIKIPDYSDFK	73
QY	59	-----WSEALQFTIRILNVH---VPRLHKXF-IAGFQVRLAAANFTFKVRAPE	106
Db	74	IKHLGKGHSYFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRLKMSG	133
QY	107	PLETLPL-VELLAOTRV-TQGSITRPVVISIACSLSFGSHANEFDGNSNTSHA--LLVLVQ	162
Db	134	NFDLSIEGMSISADLKLSGNETSGKPTTICSC---SSHINSVHVHISKSXGVLQIUQFH	190
QY	163	KHIXAVLSNKL---CLISLSLVQV-VNVHLGTLGLNPGVPESOIRYSMTSVPTVSDY	217
Db	191	KXIESALRNKNSQVEKVTNSVSKLQPYQTLPVMTKIDSVAGINTGLVAPPATTATET	250
QY	218	ISEVNVAVFLGLKPIILPTDATPVLPL-RHVGTGSMATVGLSQQLFDSALLLLOKAG	275
Db	251	LDVQMGEPYSENH-----HNPPFPADPEWMEFPAAHDRMVTGLSDYEFNTAGLVYQAG	305
QY	276	ALNLDITGQC--RSDDNLINTSALGRLLPEVAROPPEMPVVLKVLGATPVAMLHTXNA	333
Db	306	VLMKTLRDDMLPKSEKFRLLTKFTGTFLEPVAKFPK--WKIQIHVSASTPPHLSVQPT	362
QY	334	TLRLQPFVEVLATA--SNSAFQSFLDVPVVVNLRLQLSVSKVKLGQTTSVLGDVGLTAS	391
Db	363	GLTFYPADVQAFATLENSSLASLEFLIGHMTTGSMEVSAESNRLVGEULK-LDRLLLELKH	421
QY	392	SNKGFDITDQVRLMWTVEFEKLLOHNLALLAMGIALPGVNLHVVAPEIFYEGYVVIS	451
Db	422	SNLGPPFVELLODINNTIVPLVPRVNEKLOKGFPLETPARVQIYNVVLQPHFLLFG	481
QY	452	SGLFYQ	457
Db	482	ADVVK	487

RESULT 4

US-08-072-063-2
Sequence 2, Application US/08072063
Patent No. 5439807
GENERAL INFORMATION:
APPLICANT: Theofan, Georgia
APPLICANT: Grinna, Lynn S
APPLICANT: Horwitz, Arnold
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marstall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072, 063
FILING DATE: 19930519
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 30659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-212-132-2

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLLALLPVVGASTPGTVRLNKAALSYVEIGKAPLQAL-QVTVPHELD--- 58
Db 15 WVS-LMWLVIAIGTAVTAANVPGVVRISQKGLDYASQOQTAALQKELKIKIPDYSDFK 73
QY 59 -----WSGALQPTRIRILNVH---VPRHLKF-IAGFGRVLLAAANFTFKVRAPE 106
Db 74 IXLGKGHYFSYMDIREFQPSQISVMVNLKFSISNANIKISGKKAQKRFKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHA--LLVLVQ 162
Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSSC---SSHINSVHVHISKSKVGLLQLFH 190
QY 163 KHIAVLSNKL-----CLISINLVQGVNVLHGTGLNLPVGPESQIRYSMVSVPTVTSY 217
Db 191 KKIESALRNKMSQVCEKVTNSVSKLQFYFQTLPMTKIDSVAGINYLGLVAPPATTAE 250
QY 218 ISLEYNVFLILGKPIILLPTDTPFVLP--RHVGTEGSMATVGLSQQLFDSALLLQKAG 275
Db 251 LDVQMKGEFYSNH-----HNPPFPAPVMEFPAADRNVYLGSDYFFNTAGLVYQEAG 305
QY 276 ALNLDITQL--RSDNLLNTSALGRLEPEVARQPEPMPVVLKVLGATPVAMLNTNNA 333
Db 306 VLKMTLRDDMIPKESKFRLLTKFFGTFLEPAKKEPN---MKIQIHVSASTPPLSVQPT 362
QY 334 TLRLQPFVEVLATA--SNSAFQSLSDVNNLRQLSVKVLQGTTSVLGDVQVLTAS 391
Db 363 GLTFYPAVDVQAFVLPNSLSLASFLIGXHTTGSMESVSAESNRLVGELK-LDRLLLELKH 421
QY 392 SNVGFIDTDQVRLTGMGTVEKPEPLLDHNLALLAMGIALPGVNNLHYVAPFIFFVEGVVVIS 451
Db 422 SNIGFPFVELLDQIMNYIPIVLPRVNEKLGKGFPLTPPARVOLYNVVLQPHQNFLLFG 481
QY 452 SGLFYQ 457
Db 482 ADVVYK 487

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RESULT 6

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US-08-414-924-2
; Sequence 2, Application US/08414924
; Patent No. 5494896
; GENERAL INFORMATION:
; APPLICANT: Hansbrough, John F.
; TITLE OF INVENTION: Method of Treating Conditions
; TITLE OF INVENTION: Associated With Burn Injuries
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

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; ZIP: 60606-6432
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,924
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-414-924-2

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Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLLALLPVVGASTPGTVRLNKAALSYVEIGKAPLQAL-QVTVPHELD--- 58
Db 15 WVS-LMWLVIAIGTAVTAANVPGVVRISQKGLDYASQOQTAALQKELKIKIPDYSDFK 73
QY 59 -----WSGALQPTRIRILNVH---VPRHLKF-IAGFGRVLLAAANFTFKVRAPE 106
Db 74 IXLGKGHYFSYMDIREFQPSQISVMVNLKFSISNANIKISGKKAQKRFKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHA--LLVLVQ 162
Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSSC---SSHINSVHVHISKSKVGLLQLFH 190
QY 163 KHIAVLSNKL-----CLISINLVQGVNVLHGTGLNLPVGPESQIRYSMVSVPTVTSY 217
Db 191 KKIESALRNKMSQVCEKVTNSVSKLQFYFQTLPMTKIDSVAGINYLGLVAPPATTAE 250
QY 218 ISLEYNVFLILGKPIILLPTDTPFVLP--RHVGTEGSMATVGLSQQLFDSALLLQKAG 275
Db 251 LDVQMKGEFYSNH-----HNPPFPAPVMEFPAADRNVYLGSDYFFNTAGLVYQEAG 305
QY 276 ALNLDITQL--RSDNLLNTSALGRLEPEVARQPEPMPVVLKVLGATPVAMLNTNNA 333
Db 306 VLKMTLRDDMIPKESKFRLLTKFFGTFLEPAKKEPN---MKIQIHVSASTPPLSVQPT 362
QY 334 TLRLQPFVEVLATA--SNSAFQSLSDVNNLRQLSVKVLQGTTSVLGDVQVLTAS 391
Db 363 GLTFYPAVDVQAFVLPNSLSLASFLIGXHTTGSMESVSAESNRLVGELK-LDRLLLELKH 421
QY 392 SNVGFIDTDQVRLTGMGTVEKPEPLLDHNLALLAMGIALPGVNNLHYVAPFIFFVEGVVVIS 451
Db 422 SNIGFPFVELLDQIMNYIPIVLPRVNEKLGKGFPLTPPARVOLYNVVLQPHQNFLLFG 481
QY 452 SGLFYQ 457
Db 482 ADVVYK 487

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RESULT 7

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US-08-311-611A-69
; Sequence 69, Application US/08311611A
; Patent No. 5523288
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan

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1 APPLICANT: Kung, Ada H.C.
2 APPLICANT: Lambert, Jr., Lewis H.
3 TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
4 TITLE OF INVENTION: Infection by Administration of
5 TITLE OF INVENTION: Bactericidal/Permeability-Increasing
6 TITLE OF INVENTION:
7 NUMBER OF SEQUENCES: 227
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
10 STREET: 6300 Sears Tower, 233 South Wacker Drive
11 CITY: Chicago
12 STATE: Illinois
13 COUNTRY: USA
14 ZIP: 60606-6402
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent in Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/311.611A
22 FILING DATE:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 08/273,401
25 FILING DATE: 11-JUL-1994
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/125,651
28 FILING DATE: 22-SEP-1993
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Sharp, Jeffrey S.
31 REGISTRATION NUMBER: 31,879
32 REFERENCE/DOCKET NUMBER: 32251
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 312/474-6300
35 TELEFAX: 312/474-0448
36 TELEX: 25-3856
37 INFORMATION FOR SEQ ID NO: 69:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 487 amino acids
40 TYPE: amino acid
41 TOPOLOGY: linear
42 MOLECULE TYPE: protein
43 FEATURE:
44 NAME/KEY: misc feature
45 OTHER INFORMATION: "r3PI"
46 US-08-311-611A-69
47
48 Query Match 12.5%; Score 283; DB 1; Length 487;
49 Best Local Similarity 22.4%; Pred. No. 6.5e-21;
50 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;
51
52 QY 3 WASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHELD--- 58
53 DB 15 WVS-LMWLVAGTAVTAANPGVWVRISQKGLDYASQOQTAALQKELKRIKIPYSDSFK 73
54
55 QY 59 -----MSGEALQPTRILNVH---VPRHLKE-IAGFGVRLAAANFTKVRAP 106
56 DB 74 IKHLGKHGHSFYSDMDEEQLPSSQISWPNVGLKFSINANKISGKWKAKRFLKMG 133
57 QY 107 PLELTLP-VELLADTRV-TOSSIRTPVWSISACLSFGSHANEPDGSNSTSHA--LLVLVQ 162
58 DB 134 NFDLSIEGMSIGADLKLGNPTSGKPTITCSSC---SSHINSVHVHHSKVKGNLQLFH 190
59 QY 163 KHKAVLSNKL-----CLISINLVQG-VNVLHGLIGLNPVGPESQIRYSWVPTVTSY 217
60 DB 191 KKIESALRNKMSQVCEKVTNSVSSKLQFYFQTLPMVKIDSVAGINYLGAAPPATTAT 250
61 QY 218 ISLEVNANVLLGKPIILPTDTPFVLP--RVVGTGSMATVCLSQOLFDSALLILQKAG 275
62 DB 251 LDVQKGEFYSNH-----HNPPFPAPPVPEPAAHDMVVLGSLDYFFNTAGLVQEQAG 305
63 QY 276 ALNLDITGOL--RSDNLTNTSALGLRIPEVARQFPPEPMPVVLKVRIGATPVANLHTNNA 333
64
65 Db 306 VLKMTLDDDWIPKESXFLRTTKFFGTFLPEVAKFPN---MKIQIHVSASTPEHLSVQPT 362
66 QY 334 TLRLQPFVEVLATA--SNSAFQSLFSLDVVVNRLQLSVSKVLQGTTSVLGDLVLTWAS 391
67 Db 363 GLTFPAVDVQAFVLPNSLASLFLIGHHTTGSMEVSAESNELVGLK-LDRLLLELKH 421
68 QY 392 SNVGFIDTDQVRLMTGTFVEKPLDHLNALLAMGIALPGVWNLHYVAPEIFVVEGYVWIS 451
69 Db 422 SNIGFPFVELLODINKYIVPILVPRVNEKLGKGFPLTPARVOLNPNVZQPHQNFLEFG 481
70 QY 452 SGLFYQ 457
71 Db 482 ADWVYK 487
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73 RESULT 8
74 US-08-311-611A-146
75 ; Sequence 146, Application US/08311611A
76 ; Patent No. 5523288
77 ; GENERAL INFORMATION:
78 ; APPLICANT: Cohen, Jonathan
79 ; APPLICANT: Kung, Ada H.C.
80 ; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
81 ; TITLE OF INVENTION: Infection by Administration of
82 ; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
83 ; TITLE OF INVENTION:
84 ; NUMBER OF SEQUENCES: 227
85 ; CORRESPONDENCE ADDRESS:
86 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
87 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
88 ; CITY: Chicago
89 ; STATE: Illinois
90 ; COUNTRY: USA
91 ; ZIP: 60606-6402
92 ; COMPUTER READABLE FORM:
93 ; MEDIUM TYPE: Floppy disk
94 ; COMPUTER: IBM PC compatible
95 ; OPERATING SYSTEM: PC-DOS/MS-DOS
96 ; SOFTWARE: Patent in Release #1.0, Version #1.25
97 ; CURRENT APPLICATION DATA:
98 ; APPLICATION NUMBER: US/08/311.611A
99 ; FILING DATE:
100 ; PRIOR APPLICATION DATA:
101 ; APPLICATION NUMBER: 08/273,401
102 ; FILING DATE: 11-JUL-1994
103 ; PRIOR APPLICATION DATA:
104 ; APPLICATION NUMBER: 08/125,651
105 ; FILING DATE: 22-SEP-1993
106 ; ATTORNEY/AGENT INFORMATION:
107 ; NAME: Sharp, Jeffrey S.
108 ; REGISTRATION NUMBER: 31,879
109 ; REFERENCE/DOCKET NUMBER: 32251
110 ; TELECOMMUNICATION INFORMATION:
111 ; TELEPHONE: 312/474-6300
112 ; TELEFAX: 312/474-0448
113 ; TELEX: 25-3856
114 ; INFORMATION FOR SEQ ID NO: 146:
115 ; SEQUENCE CHARACTERISTICS:
116 ; LENGTH: 487 amino acids
117 ; TYPE: amino acid
118 ; TOPOLOGY: linear
119 ; MOLECULE TYPE: protein
120 ; FEATURE:
121 ; NAME/KEY: misc feature
122 ; OTHER INFORMATION: "r3PI"
123 ; US-08-311-611A-146
124
125 Query Match 12.5%; Score 283; DB 1; Length 487;
126 Best Local Similarity 22.4%; Pred. No. 6.5e-21;
127 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;
128
129 QY 3 WASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHELD--- 58
130 DB 15 WVS-LMWLVAGTAVTAANPGVWVRISQKGLDYASQOQTAALQKELKRIKIPYSDSFK 73
131
132 QY 59 -----MSGEALQPTRILNVH---VPRHLKE-IAGFGVRLAAANFTKVRAP 106
133 DB 74 IKHLGKHGHSFYSDMDEEQLPSSQISWPNVGLKFSINANKISGKWKAKRFLKMG 133
134 QY 107 PLELTLP-VELLADTRV-TOSSIRTPVWSISACLSFGSHANEPDGSNSTSHA--LLVLVQ 162
135 DB 134 NFDLSIEGMSIGADLKLGNPTSGKPTITCSSC---SSHINSVHVHHSKVKGNLQLFH 190
136 QY 163 KHKAVLSNKL-----CLISINLVQG-VNVLHGLIGLNPVGPESQIRYSWVPTVTSY 217
137 DB 191 KKIESALRNKMSQVCEKVTNSVSSKLQFYFQTLPMVKIDSVAGINYLGAAPPATTAT 250
138 QY 218 ISLEVNANVLLGKPIILPTDTPFVLP--RVVGTGSMATVCLSQOLFDSALLILQKAG 275
139 DB 251 LDVQKGEFYSNH-----HNPPFPAPPVPEPAAHDMVVLGSLDYFFNTAGLVQEQAG 305
140 QY 276 ALNLDITGOL--RSDNLTNTSALGLRIPEVARQFPPEPMPVVLKVRIGATPVANLHTNNA 333
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QY 59 -----WSGEALQPTRIRILNVH---VPRHLKPF-IAGFVRLLAANFTKVFRAPE 106
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 74 IKHLGKHYFSYMDIREFOLPSSQISWVNVGLKFSISNANIKISGKWKAKQKFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVSISACSLFSGHANEFDSNSTSHA--LLVLVQ 162
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSC---SSHINSVHVHISKSKVGLIQLFH 190

QY 163 KHKAVLSNKL-----CLISNLVQGV-VNVHLGTLIGLNPVGPESQIRYSVMVSVPTVTSY 217
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 191 KLESALRNKNSQVCEKVTNSVSSKLPYQTLPMVKIDSVAGINGLVAPPAITTAET 250

QY 218 ISLEVNVLFLGKPIILPTDTPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 251 LDVQMKGEFYSNH-----HNPPFPAPVMEFPAADHDMVVLGLSDYFFNTAGLVYQAG 305

QY 276 ALNLDTITQGL--RSDDNLNLTSALEGLIPEVAROPPEPMPVWLKVRGLGATPVAMLHTNNA 333
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 306 VLKMTLRDDMIPKSKPRLLTKFFGTFLPEVAKFPN---MKIQHVSASTPPHLSVQPT 362

QY 334 TLRQPFVEVLATA--SNSAFQSLFSLDVVNVNLRQLSVSKVKLQGTTSVLGVDVLTVAS 391
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 363 GLTFYPAVDVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421

QY 392 SNVGFIDTQVRLMTGTVFEKPLDLHNLALLANGIALPGVNVHVAPEIFVYEGYVVIS 451
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 422 SNIGFPFVELLDIMNYIVPILVRVNEKIQKGFPLTPARVQLYNNVLQPHQNFLLFG 481

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 482 ADVYIK 487

RESULT 9

US-08-173-968-2
; Sequence 2, Application US/08173968
; Patent No. 5576292
; GENERAL INFORMATION:
; APPLICANT: Elsbach, Peter
; APPLICANT: Weiss, Jerrold
; TITLE OF INVENTION: Biologically Active
; TITLE OF INVENTION: Bactericidal/Permeability-increasing Protein Fragments
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howard M. Frankfort
; STREET: 805 Third Ave.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,968
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/754,204
; FILING DATE: 26-AUG-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Frankfort, Howard M.
; REGISTRATION NUMBER: 32,613
; REFERENCE/DOCKET NUMBER: 5969/05982US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELE: 236687
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Query Match 12.5%; Score 283; DB 1; Length 487;

Best local Similarity 22.4%; Ered. No. 6.5e-21;

Matches 103; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLLALLLPVVGASTFGTVVRLNKAALSYSVSEIGKAPLQAL--QVTVPHFLD--- 58
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
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; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 15 WVS-LMVVAIGTAVTAANVGVVVRISOKGLDVASQQTAAALQKELKRIKIPDYSDFX 73

QY 59 -----WSGEALQPTRIRILNVH---VPRHLKPF-IAGFVRLLAANFTKVFRAPE 106
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 74 IKHLGKHYFSYMDIREFOLPSSQISWVNVGLKFSISNANIKISGKWKAKQKFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVSISACSLFSGHANEFDSNSTSHA--LLVLVQ 162
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSC---SSHINSVHVHISKSKVGLIQLFH 190

QY 163 KHKAVLSNKL-----CLISNLVQGV-VNVHLGTLIGLNPVGPESQIRYSVMVSVPTVTSY 217
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 191 KLESALRNKNSQVCEKVTNSVSSKLPYQTLPMVKIDSVAGINGLVAPPAITTAET 250

QY 218 ISLEVNVLFLGKPIILPTDTPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 251 LDVQMKGEFYSNH-----HNPPFPAPVMEFPAADHDMVVLGLSDYFFNTAGLVYQAG 305

QY 276 ALNLDTITQGL--RSDDNLNLTSALEGLIPEVAROPPEPMPVWLKVRGLGATPVAMLHTNNA 333
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 306 VLKMTLRDDMIPKSKPRLLTKFFGTFLPEVAKFPN---MKIQHVSASTPPHLSVQPT 362

QY 334 TLRQPFVEVLATA--SNSAFQSLFSLDVVNVNLRQLSVSKVKLQGTTSVLGVDVLTVAS 391
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 363 GLTFYPAVDVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 422 SNIGFPFVELLDIMNYIVPILVRVNEKIQKGFPLTPARVQLYNNVLQPHQNFLLFG 481

QY 452 SGLFYQ 457
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

Db 482 ADVYIK 487

RESULT 10

US-08-232-527-2
; Sequence 2, Application US/08232527
; Patent No. 5578568
; GENERAL INFORMATION:
; APPLICANT: Ammons, William Steve et al.
; TITLE OF INVENTION: Method of Treating Conditions Associated with
; TITLE OF INVENTION: Intestinal Ischemia/Reperfusion
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,527
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-232-527-2

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 103; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

Qy 3 WASRLGLLJALLPVVGASTGTVRLNKAALSYVSEIGKAPLQAL-QVTVPHEFLD--- 58
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15 WVS-LMVLVAIGTAVTAANPGVVRISQKGLDYASQQTALQKELKRIKIPYSDSEFK 73
Qy 59 -----WSEALQPTRIRILNVE---VPRHLKF-IAGFGVRLLAANFTFKVRAPE 106
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
74 IKHLGKHYSFYSDIREFQLPSSQISMVNVGLKFSISNANIKISGKKAQKFLKMSG 133
Qy 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANEPDGSNSTSHA--LLVLVQ 162
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
134 NFDLSIEGMSIADLKLGSNFTSGKPIITCSC---SSHINSVHVHISKVGVLIQLFH 190
Qy 163 KHKAVLSNKL-----CLSIHNLVQGVNVHLGTILGNPVGPEQIRYSVMYVPTVTSY 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 KTIESALRNKNSQVCEKVTNSVSKLQPYQTLPVMTKIDSVAGINYLVPAPPTAET 250
Qy 218 ISLEVNNAVLLGKPIILPTDTPFVLP--RHVTEGSMATVGLSQQLFDSALLLQKAG 275
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 LDVQMKGEFYSENH-----HNPPFPAPVMEFPAADRMMVYGLSDYFNTAGLIVYQEAG 305
Qy 276 ALNLDTGQL--RSDNLLNTSALGRLLPEVAROPPEPMPVVLKVRIGATPVAMLHTNNA 333
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 VAKTLRDDMTPKESKRLTKFTGTLPVAKKFPN---MKIQIHVSASTPPLHSVQPT 362
Qy 334 TLRQPFVEVLATA--SNSAFQSLFSLDVVNLRLQLSVSKVKGTTSLVGLDVOLTVAS 391
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363 GL-FYPAVDVQAFVAVLNSLSLFL-GMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421
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422 SN-GPFFVELLQDLMNVIVPLVLRVNEKLGKQFPPLTPARVQLVNVVLPQHQNFLLFG 481
Qy 452 SGLFYQ 457
Db : : : : :
482 ADVYK 487

RESULT 11
US-08-372-783-69
; Sequence 69, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; MATERIALS
; NUMBER OF SEQUENCES: 237
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```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; APPLICATION DATA:
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Heien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "rBPI"
; US-08-372-783-69

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 103; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

Qy 3 WASRLGLLJALLPVVGASTGTVRLNKAALSYVSEIGKAPLQAL-QVTVPHEFLD--- 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
15 WVS-LMVLVAIGTAVTAANPGVVRISQKGLDYASQQTALQKELKRIKIPYSDSEFK 73
Qy 59 -----WSEALQPTRIRILNVE---VPRHLKF-IAGFGVRLLAANFTFKVRAPE 106
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
74 IKHLGKHYSFYSDIREFQLPSSQISMVNVGLKFSISNANIKISGKKAQKFLKMSG 133
Qy 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANEPDGSNSTSHA--LLVLVQ 162
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134 NFDLSIEGMSIADLKLGSNFTSGKPIITCSC---SSHINSVHVHISKVGVLIQLFH 190
Qy 163 KHKAVLSNKL-----CLSIHNLVQGVNVHLGTILGNPVGPEQIRYSVMYVPTVTSY 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 KTIESALRNKNSQVCEKVTNSVSKLQPYQTLPVMTKIDSVAGINYLVPAPPTAET 250
Qy 218 ISLEVNNAVLLGKPIILPTDTPFVLP--RHVTEGSMATVGLSQQLFDSALLLQKAG 275
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 LDVQMKGEFYSENH-----HNPPFPAPVMEFPAADRMMVYGLSDYFNTAGLIVYQEAG 305
Qy 276 ALNLDTGQL--RSDNLLNTSALGRLLPEVAROPPEPMPVVLKVRIGATPVAMLHTNNA 333
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 VAKTLRDDMTPKESKRLTKFTGTLPVAKKFPN---MKIQIHVSASTPPLHSVQPT 362
Qy 334 TLRQPFVEVLATA--SNSAFQSLFSLDVVNLRLQLSVSKVKGTTSLVGLDVOLTVAS 391
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
363 GL-FYPAVDVQAFVAVLNSLSLFL-GMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421
Qy 392 SNVGFIDTQVTLGVTGFEKPLDHLNALLAMGIALPGVNVLFVAPFIVGVYVVIS 451
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
422 SN-GPFFVELLQDLMNVIVPLVLRVNEKLGKQFPPLTPARVQLVNVVLPQHQNFLLFG 481
Qy 452 SGLFYQ 457
Db : : : : :
482 ADVYK 487
```


363 GLTFYPAVDVQAFVAVLNNSSLASLFLICMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421
392 SNVGFIDTQVRLMGTVFEKPLDLHALLAMGIALPGVNLHYVAPEIFVYGVVIS 451
422 SNIGFFVLLQDIMNVIPIVILPRVNEKLGKGFPLTPARVQLYNNVLIQPHQNFLLFG 481
452 SGLFYQ 457
482 ADVYK 487

RESULT 12
US-08-372-783-146
; Sequence 146, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-372-783-146

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 183; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

3 WASRLGILLALLPVVCASTGTVVRLNKAALSIVSEIGKAPLORAL-QTVVPHFLD--- 58
15 WWS-LMWLVAVGTAVTAANPVGVVVRISQQGLDYASQQGTAALQKELKRIKIPYDSDFX 73
59 -----NSGEALQPTRILNVH---VPLRLKF-IAGFGVRLLAANFTKVFRAPE 106
74 IKHLGKHYSFYSMIDREFQLPSSQISMVNVGLKFSISNANIKISKWKAQRFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISIACSLSFSGHANEFDGSNSTSHA--LLVLVQ 162
DB 134 NFDUSIGMSISADLKIGSNFTSKPTITCSC---SSHINSVHVHISKSKVGMILQLPH 190
QY 163 KHIKAVLSNKL---CLISINLVQ--VNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSY 217
DB 191 KXIESALRNKMSQVCEKVTNSVSKLQPYQTLPVMTKIDSVAGINYLVAPEATTAE 250
QY 218 ISLEVNVLFLGKPIILPTDTPVLP--RHVTEGSMATVGLSQQFLDSALLLQKAG 275
DB 251 LDVQMGFEYSNH-----HNPPFPAPVMEFPAADRMYVLGLSDYFFNTAGLVYQAG 305
QY 276 ALNLDITQQL--RSDNLLNTSALGRILPEVAROPPEPMPVVLKVRLGATPVAMLHTNNA 333
DB 306 VLKWLIRDDMIPKESKFLTKFPGTFLPEVAKKFPN---MKIQHVSASTPPLHSVQPT 362
QY 334 TRLQPFVVLATA--SNSAFQSLFSDVWVNLQLSVSKVLOGTTSVLGDVOLTVAS 391
DB 363 GLTFYPAVDVQAFVAVLNNSSLASLFLICMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421
QY 392 SNVGFIDTQVRLMGTVFEKPLDLHALLAMGIALPGVNLHYVAPEIFVYGVVIS 451
DB 422 SNIGFFVLLQDIMNVIPIVILPRVNEKLGKGFPLTPARVQLYNNVLIQPHQNFLLFG 481
QY 452 SGLFYQ 457
DB 482 ADVYK 487

RESULT 13
US-08-372-105-69
; Sequence 69, Application US/08372105
; Patent No. 5627153
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Lim, Edward
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: Anti-Fungal Materials and Methods
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,105
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 487 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: "BPI"
 US-08-372-105-69

Query Match 12.5%; Score 283; DB 1; Length 487;
 Best Local Similarity 22.4%; Pred. No. 6.5e-21;
 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTGTVVRLNKAALSYVSEIGKAPLORAL-QVTVPHLD--- 58
 DB 15 WVS-LMWLVAGTAVTAANVPGVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSK 73

QY 59 -----WSGEALQPTRIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106
 DB 74 IKHLGKHGVSFYSDIREFQLPSSQISWVPVNGLAFSISNANIKISGKWKAKRFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANFDSNSTSHA--LLVLVQ 162
 DB 134 NFDLSIEGMSISADLKLSNPTSGKPTTICSSC---SSHINSVHVHISKSKVGLIQLFH 190

QY 163 KHIAVLSNKL-----CLISNLVQV-VNVLGTLGLNLPVGPESQIRYSMWVSVPTVSDY 217
 DB 191 KKIESALRNKNSQVCEKVTNSVSKLQPYFOTLPWTKIDSVAGINYLGLVAPPATTAT 250

QY 218 ISLEVNVLFLGKPIILPTDAPFVLP--RHVGTEGSMATVGLSQQLFDSALLLQKAG 275
 DB 251 LDVQMKGEFYSFNH-----HNPPFPAPVMEPPAAHDMVYLGLSDYPENTAGLVYQVAG 305

QY 334 TLRLQPFVEVLATA--SNSAFQSLFSLDVVNLRLQLSVSKVKLOGTTSVLGDVQITVAS 391
 DB 363 GLTFYPAVDVQAFVLPNSSLASLELIGHHTTGSMEVSAESNRLVGELK-LDRILLELKH 421

QY 392 SNVGFIDTDQVRLTLMGTVEKPELIDHLLNALLAMGIALPGVNLHYVAPEIFYEGYVVIS 451
 DB 422 SNIGFPFVELLQDMNYIVPILVLRVNEKLGKGFPLTPARVQLNVVVLQEQHNFLLFG 481

QY 452 SGLFYQ 457
 DB 482 ADVYK 487

RESULT 14

US-08-372-105-146

Sequence 146, Application US/08372105

Patent No. 5627153

GENERAL INFORMATION:

APPLICANT: Little, Roger G.

APPLICANT: Lim, Edward

APPLICANT: Lambert, Lewis H.

APPLICANT: Scannon, Patrick J.

TITLE OF INVENTION: Anti-Fungal Materials and Methods

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/372,105

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ric-Laures, Li-Hsien

REGISTRATION NUMBER: 33,547

REFERENCE/DOCKET NUMBER: 27129/32415

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-372-105-146

Query Match 12.5%; Score 283; DB 1; Length 487;

Best Local Similarity 22.4%; Pred. No. 6.5e-21;

Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTGTVVRLNKAALSYVSEIGKAPLORAL-QVTVPHLD--- 58
 DB 15 WVS-LMWLVAGTAVTAANVPGVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSK 73

QY 59 -----WSGEALQPTRIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106
 DB 74 IKHLGKHGVSFYSDIREFQLPSSQISWVPVNGLAFSISNANIKISGKWKAKRFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANFDSNSTSHA--LLVLVQ 162
 DB 134 NFDLSIEGMSISADLKLSNPTSGKPTTICSSC---SSHINSVHVHISKSKVGLIQLFH 190

QY 163 KHIAVLSNKL-----CLISNLVQV-VNVLGTLGLNLPVGPESQIRYSMWVSVPTVSDY 217
 DB 191 KKIESALRNKNSQVCEKVTNSVSKLQPYFOTLPWTKIDSVAGINYLGLVAPPATTAT 250

QY 218 ISLEVNVLFLGKPIILPTDAPFVLP--RHVGTEGSMATVGLSQQLFDSALLLQKAG 275
 DB 251 LDVQMKGEFYSFNH-----HNPPFPAPVMEPPAAHDMVYLGLSDYPENTAGLVYQVAG 305

QY 276 ALNLDITQL--RSDNLLNTSALGRILPEVARQPEPMPVVLKVRIGATPVAMLHTNNA 333
 DB 306 VLKMTLRDNDTPKESKFLTTKFFGTFLPEVAKKFPN---MKIQIHVSASTPEHLSVQPT 362

QY 334 TLRLQPFVEVLATA--SNSAFQSLFSLDVVNLRLQLSVSKVKLOGTTSVLGDVQITVAS 391
 DB 363 GLTFYPAVDVQAFVLPNSSLASLELIGHHTTGSMEVSAESNRLVGELK-LDRILLELKH 421

QY 392 SNVGFIDTDQVRLTLMGTVEKPELIDHLLNALLAMGIALPGVNLHYVAPEIFYEGYVVIS 451
 DB 422 SNIGFPFVELLQDMNYIVPILVLRVNEKLGKGFPLTPARVQLNVVVLQEQHNFLLFG 481

QY 452 SGLFYQ 457
 DB 482 ADVYK 487

RESULT 15

US-08-415-158-2

? Sequence 2, Application US/08415158
? Patent No. 5639727
? GENERAL INFORMATION:
? APPLICANT: Little, Roger G. II
? APPLICANT: Gazzano-Santoro, Helene
? APPLICANT: Parent, James Brian
? TITLE OF INVENTION: Therapeutic uses of
? TITLE OF INVENTION: Bactericidal/Pertussis-Increasing Protein Products
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
? STREET: 6300 Sears Tower, 233 South Wacker Drive
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/415,158
? FILING DATE:
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/093,202
? FILING DATE:
? APPLICATION NUMBER: US 08/030,644
? FILING DATE: 12-MAR-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Sharp, Jeffrey S.
? REGISTRATION NUMBER: 31,879
? REFERENCE/DOCKET NUMBER: 31580
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6300
? TELEFAX: 312/474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 487 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-415-158-2

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;
QY 3 WASRIGLALLLPVVGASTFTGVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58
DB 15 WVS-LMWLVAGTAAVAVNPGVVVRIQKGLDYASQQTAALQKELKRIKIPDYSDFK 73
QY 59 -----WSEALQPTIRILNVH--VPRHLKF-IAGFGVRLLAANFTFKVFRAP 106
DB 74 IKHLGKHYSFYSDMIREFQPSQISMVNVLKFSISNANIKISGKWKAKRFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANEFDSNSTSHA--LLVLVQ 162
DB 134 NFDLSIEGMSIADLKLSGNFTSGKPTTCSCC---SSHINSVHVHISKSKVGLIQLFH 190
QY 163 KHIKAVLSNKL-----CLISNLVQG-VNVHGLTGLGNPVGPESQIRYSMVSVPTVTSY 217
DB 191 KKIESALRNKNSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLVAAPPATTAT 250
QY 218 ISLENAVLELLGKPIILLPTDAPVLP--RHVGTGSMATVGLSQQLFDSNALLLQKAG 275
DB 251 LDVQMKGEFYSENH-----HNPPFPAPVMEFPAAHDMVYLGSLDYFFNTAGLYVQ 305
QY 276 ALNLDITQL--RSDNLTNSALGRLLPEVARQFPEMPVVLKVLGATPVAMLHTNNA 333
DB 306 VLKWLTRDDMPKESKRLTKFTFELPEVAKFNP---MKIQLHVSASTPPELSVQPT 362

QY 334 TLRLOPFVEVLATA--SNSAFQSLFSLDWWVNLRLQLSVSKVKLQQTTSVLGDVOLTVAS 391
DB 363 GLTFYPAVDVQAFVLPNSSLASLFLIGHMTGSEVSAESNRLVGLK-LDRLLLELKH 421
QY 392 SNVGEIDTDQVRLTMGTVFEXPLLDHLNALALAMGIALPGVNLHVTVAPEIFYEGYVVIS 451
DB 422 SNIGFPFVELLDIMNYIVPILVLPVNEKLGKGFPLTPARVOLYNNVVLPQHPNELLFG 481
QY 452 SGLFYQ 457
DB 482 ADVVYK 487

Search completed: June 29, 2004, 11:01:30
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2004, 10:56:44 ; Search time 21 Seconds
(without alignments)
2097.891 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265
Sequence: - MAWASRLGULLALLPFWGA.....PEIFVYEGYVWISSGLFYQS 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listings first 45 summaries

Database : PIR 78:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	392.5	17.3	470	2	S17447	probable ligand-bi
2	353	15.6	473	2	S17448	probable ligand-bi
3	283	12.5	487	2	A30909	bactericidal/perme
4	256	11.3	481	2	A54136	lipopolysaccharide
5	251	11.1	482	2	B35843	lipopolysaccharide
6	247.5	10.9	482	2	S10190	bactericidal perme
7	246.5	10.9	481	2	I56246	lipopolysaccharide
8	241	10.6	477	2	A35843	lipopolysaccharide
9	173	7.6	493	2	I49370	plasma phospholipi
10	159.5	7.0	493	2	A53533	phospholipid trans
11	132	5.8	250	4	S43383	bactericidal/perme
12	132	5.8	576	2	T22700	hypothetical prote
13	120.5	5.3	488	2	C86183	hypothetical prote
14	116	5.1	606	2	T29190	hypothetical prote
15	113	5.0	974	2	A90140	conserved hypothet
16	112	4.9	554	2	T15438	hypothetical prote
17	111	4.9	493	2	A53176	cholesterol ester
18	109.5	4.8	1131	2	T41144	hypothetical serin
19	109.5	4.8	1749	2	S75071	hypothetical prote
20	109	4.8	4436	2	E71086	hypothetical prote
21	105.5	4.7	553	2	A81057	hypothetical integ
22	105	4.6	4152	2	T31102	filamentous hemagg
23	104	4.6	1455	2	F88941	protein R13D1.7
24	103.5	4.6	1176	2	T18042	ice nucleation pro
25	103	4.5	488	2	D64108	glucuronate transp
26	103	4.5	766	2	T07171	subtilisin-like pr
27	102.5	4.5	812	2	T39817	hypothetical prote
28	102.5	4.5	1118	1	SYBYCP	carbamoyl-phosphat
29	102	4.5	637	2	A54000	sodium/phosphate c

ALIGNMENTS

RESULT 1

S17447

probable ligand-binding protein RY2G5 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence_revision 22-May-1998 #text_change 05-Nov-1999

C:Accession: S17447

R:Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.

EMBO J. 10, 2813-2819, 1991

A:Title: Novel genes for potential ligand-binding proteins in subregions of the olfacto:

A:Reference number: S17447; MUID:92007724; PMID:1915264

A:Accession: S17447

A:Molecule type: mRNA

A:Residues: 1-470 <DEA>

A:Cross-references: EMBL:X60660; NID:g57731; PIDN:CAA43067.1; PID:g57732

A:Experimental source: Olfactory mucosa

C:Genetics:

A:Gene: RY2G5

C:Keywords: olfaction

Query Match 17.3%; Score 392.5; DB 2; Length 470;
Best Local Similarity 26.9%; Pred. No. 66-22;
Matches 109; Conservative 81; Mismatches 182; Indels 33; Gaps 5;

Qy	67	TRIRLNHVPRHLRKFIAAGVRLAAANFTKVFRAPELELTLPVELADTRVTQSS	126
Db	80	TGLRIVELTLPYRSVRLPGVYLSYTYVAINGKS-IGFLDIAYEVNITAKVRLTMDR	139
Qy	127	IRTPVVSISACSLPSGH-----ANFDGSNSTSHALLVLQKHKAVLSNKLCLS	176
Db	140	TGYPRLVIERCDTLGGIKVKLRGLLPNLDN-----LNRVLANVLPLDLCPI	189
Qy	177	ISNLVQGVNVHLTGLGLNPVGPESQIRYSMSVPTVTSDYISLEVNAY-----F	227
Db	190	VYVVLGVNDQLGLVDSVPLGILGSVYTFSSPLVTGFELELDLNTLVGEAGDLIDY	249
Qy	228	LLGKPIILTDATPPVLPVRHVTGEGSMATVGLSQQLFDSALLTIQKAGANLDTITGOLS	287
Db	250	PLGRPAMLPQPMPELPPMGDNTNSQLA---ISANFLSSVLTMLQKQALDIDITDGMFE	306
Qy	288	DNMLNTSALGRILPEVAQFPEPMVILKVRIGATPVAMLHTNNATLRLOPFVEVJATA	347
Db	307	DLPLPLTSTLGLIPKVFQYPSRPLTIRIQPNPPTVTTLQDKALKVKVFATSEVVWSQ	366
Qy	348	SNSAFQSLSLDWNLRQLSVSKVKLOGTTSVLGDVQLTVASSNVGFEIDTVQVRLKG	407
Db	367	PNVETTCILVDITDILLASFSEVGDKLM-IDAKLQKTSUNGTSNVGNPVDVILEMLVE	425
Qy	408	TVFEKPLDLHLLNALLAMGIALPGVNLHYVAPEIFVYEGVWISS	452
Db	426	KIFDLAFPMANAILGSGVPLPKILNIDFSNADIDVLELLVLST	470

30	101.5	4.5	498	2	AD0854	probable permease
31	101.5	4.5	637	2	S01509	NADH2 dehydrogenas
32	101	4.5	487	2	T18952	hypothetical prote
33	101	4.5	523	2	T08854	dihydrolipoamide d
34	100	4.4	1774	2	S13178	6-methylsalicylic
35	100	4.4	2406	2	A54148	odz protein - frui
36	100	4.4	2515	2	S47008	tenascin-like prot
37	99.5	4.4	392	2	T04150	RAD23 protein homo
38	99	4.4	325	2	AF2665	conserved hypothet
39	99	4.4	333	2	E97447	hypothetical prote
40	99	4.4	430	2	G75408	probable transport
41	99	4.4	898	2	B65236	Mg(2+) transport A
42	99	4.4	898	2	C91281	Mg2+ transport ATP
43	99	4.4	898	2	D86132	Mg2+ transport ATP
44	98.5	4.3	409	2	H97889	conserved hypothet
45	98.5	4.3	707	2	JC7763	neuronal leucine-r

RESULT 2

S17448
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-374, 'L', 376-487 <WIL>
A:Experimental source: HL-60 cells
A:Note: sequence extracted from NCBI backbone (NCBI:P149855)
R:Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.
J. Biol. Chem. 262, 14891-14894, 1987
A:Title: A 25-kDa amino-terminal fragment carries all the antibacterial activities of
A:Reference number: A29464; MUID:88033057; PMID:3667613
A:Accession: A29464
A:Molecule type: protein
A:Residues: 32-51 <OOI>
A:Experimental source: neutrophils
R:Wassiluk, K.R.; Skubitz, K.M.; Gray, B.H.
Infect. Immun. 59, 4193-4200, 1991
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which
A:Reference number: A43600; MUID:92040097; PMID:1937776
A:Accession: A43600
A:Molecule type: protein
A:Residues: 32-52, 'R' <WAS>
R:Little, R.G.; Kellner, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.
J. Biol. Chem. 269, 1865-1872, 1994
A:Title: Functional domains of recombinant bactericidal/permeability increasing protein
A:Reference number: A49716; MUID:94124531; PMID:8294435
A:Accession: A49716
A:Molecule type: protein
A:Residues: 32-130, 132-141, 143-165, 202-215, 'E', 217-225 <LIT>
C:Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-
which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysacch-
between BPI and an LPS-binding protein from liver and cholesterol ester transfer prote-
C:Genetics:
A:Gene: GDB:BPI
A:Cross-references: GDB:131572; OMIM:109195
A:Map position: 20q11.23-20q12
C:Superfamily: lipopolysaccharide-binding protein
C:Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil
F:31/Domain: signal sequence #status predicted <SIG>
F:32-487/Product: bactericidal permeability-increasing protein #status predicted <MAT>
F:32-51/Region: bactericidal #status predicted
F:380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.6%; Score 353; DB 2; Length 473;
Best Local Similarity 25.3%; Pred. No. 5.9e-19;
Matches 12; Conservative 93; Mismatches 212; Indels 52; Gaps 12;
QY 9 LLLALLPVVG-ASTPGTVVRANKAALSYVSEIGKA-----FLORALQVTVPH--- 55
Db 10 LLWGLATPCGLLETVGLARIK-----DELGKAIQNSLVGCPILQNVLTGTVTSVNOG 63
QY 56 -----FLWSG-----EALOPTIRIRILNVHPRHLKPTIAGFGVRLAAANFT 98
Db 64 LLGAGLLGGGLLSYGGLFSVLEELSGLKIELT--LPTVS-KLLPGVGVL---SLHT 118
QY 99 FKVFRAPET---LELTPEVLLADTRVTCSSIRTPVWSISACLSFGSHANEFGDSNSTS 154
Db 119 KVSLEHSGPLVGLQLAAEWNSSKVALGMSPGTPIILIKRNTLGHISLTSGLLPT- 177
QY 155 HALLVLVQHXKAVLSNKLCLSLNVLQGVNVHGLTGLNPGVPSQIRYSMVSVPTVT 214
Db 178 -PIFGLVEQTLCKVPCGLPCVVDVSLVSVNELLGATLSIVZGLPGSSVEFTLTLPLIS 236
QY 215 SYVISEVNAVLT-FLGKPIILPTDTPVLPVPHVTEGSMACVGLSQQLFDSALLLQK 273
Db 237 NQYIELDINPIVKSIAAGVIDPDKPLVKMP---PKEDHTSQVTVPLVLENTVFGLLQT 293
QY 274 AGALNDITGQLRSDNLTLSALGRILPEVARQFPEPMPVILKRLGATPVAMLTNNA 333
Db 294 NGALDLITPEMVPNPIPTTDLAALAPALGKLPQGLLSLVKMSFPIILQNKV 353
QY 334 TLRLQFVFLVATASNAFQSLFSLDVVNRLQLSVSKYKLAQTTSLVDGVOLTVAASN 393
Db 354 TVSIPVTIHLVSSVPGQTPVALLFMGMVMTLNALHVPSTTKLHLSLS-LERLTVQLASSF 412
QY 394 VGFITDQVRLMGTVFEKPLDLHALLAMGIALPGVNVHLYVAPEIFYEGYGVVIS 451
Db 413 SQPFDSARLEEMLSDVVRAAYQKLEHLEVGLPKILNVNFANSDVDVNIENAVLT 470

RESULT 3

A30909
bactericidal/permeability-increasing protein precursor - human
N:Alternate names: 55k bactericidal protein
C:Species: Homo sapiens (man)
C:Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text change 20-Aug-1999
R:Gray, P.W.; Flagg, G.; Leong, S.R.; Gumina, R.J.; Weiss, J.; Ooi, C.E.; Elsbach, P.
J. Biol. Chem. 264, 9505-9509, 1989
A:Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and
A:Reference number: A33850; MUID:89255455; PMID:2722846
A:Accession: A33850
A:Molecule type: mRNA
A:Residues: 1-487 <GRA>
A:Cross-references: GB:J04739; NID:gl179528; PID:AAA51841.1; PID:gl179529
R:Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon
J. Biol. Chem. 269, 17411-17416, 1994
A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi
A:Reference number: A54136; MUID:94292492; PMID:7517398
A:Accession: B54136

Query Match 12.5%; Score 283; DB 2; Length 487;
Best Local Similarity 22.4%; Pred. No. 1.2e-13;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;
QY 3 WASRLGLLALLPVVGASTPGTVVRANKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58
Db 15 WVS-LMVLVAIGTAVTAANVPGVVVRISOKGLDYASQQGTRALQKELKRIKIPDYSDFX 73
QY 59 -----WSGEALOPTIRIRILNVH---VPRHLKF-IAAGFVRLAAANFTFKVRAPE 106
Db 74 IKHLGKHYSFYSDMIREFQSPSSQISVWPNVGLKFSNISANIKISGKNKAKRFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACLSFGSHANEFGDSNSTSHA--LLVLVQ 162
Db 134 NFDLSIEGMSIADLKLGSNPTSGKETITCSSC---SSHINSVHVHISKSVGLIQLFH 190
QY 163 KHIAKVLNKL-----CLSLNVLQGV-VNVLGTLGLNPGVPSQIRYSMVSVPTVTSY 217
Db 191 KLESALRNKMSQVCEKVTNSVSKLQFYQTLPTWKIDSVAGNYGLVAPATAET 250
QY 218 ISLEVNAILFLGKPIILPTDTPVLP--RHVGTSGMATVGLSQQLFDSALLLQKAG 275
Db 251 LQVKGKGFYSNH-----HNPPFPAPVWEPFAAHDVRLVGLSYFFENTAGLVYQEAG 305
QY 276 ALNLDITGQL--RSDNLTLSALGRILPEVARQFPEPMPVILKRLGATPVAMLTNNA 333
Db 306 VLKMTLRDMDIPKESKFRITTKFFGFLPEVAKTFN--MKIQIHVSASTPPLHSVQPT 362
QY 334 TLRLQFVFLVATA--SNSAFQSLFSLDVVNRLQLSVSKYKLAQTTSLVDGVOLTVA 391
Db 363 GLTFFPAVDVQAFVLPNSLASLFLGHMTTGSMEVSAESNRLVGELK-LDRILLELKH 421

A:Molecule type: mRNA
 A:Residues: 1-482 <LEO>
 A:Cross-references: EMBL:X52563; NID:g138; PID:CAA36797.1; PID:g139
 C:Superfamily: lipopolysaccharide-binding protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-482/Product: bactericidal permeability increasing protein #status predicted <MAT>

Query Match 10.9%; Score 247.5; DB 2; Length 482;
 Best Local Similarity 22.6%; Pred. No. 5.9e-11;
 Matches 110; Conservative 98; Mismatches 224; Indels 61; Gaps 16;

QY 3 WASRLGLLALLPVGASTPCTVRLNKAALSYVSEIGKAPLQALQ-VTVPHF-----56
 DB 11 WATL-VWLAAGTAVTTTPGIVARITQKGLDACCQGVLTQKLEKTIIPFSGNFK 68
 QY 57 LWSGEA-----LQPTRIRILNVHVPRIHLKFIAGFGVR---LAAAA 95
 DB 69 IKYLGKQYFFSMVIOGFNLNSQIRPLDPKGLDLSIRDASIKIRCKWKARKNFIXLGG 128
 QY 96 NETFKYFRAPELELTLPVELLADTRVTSQSSIRTPVVSISACSLFSG-HANEFQGSNSTS 154
 DB 129 NFOLSV-----EGISILAGNLGYPASGHST-----VTCSSCS--SGIN-VRIHISGSL 177
 QY 155 HALLVLVQKHIAVL---SNKCLSLSTSNLVQGV-VNVHLGTGLGNPVGSEIQIRYSWVS 209
 DB 178 GMLIQLFKRIEISLQKSMTRKICEVTSVSSKAPYFOTLPVTKLDKVGVDVSLVA 237
 QY 210 VFTVTSQYSLSENAVILFLG---KPIILPTDTPFVLPRHVTGEGSMATVGLSQOLF 265
 DB 238 PPRATANLTDLLKGEFFSLAHSRSPPEFAPALAF-----SDHDRVYVLGISYFFN 290
 QY 266 SALLILQKAGALNLDITGOL--RSDNLTNTSALGRILPEVARQPPPEPVPVVKVRLGAT 323
 DB 291 TAGFVYQKAGALNLTDDIMPKESFRITTKFFGLIPQVAKMFPD-MQMQLFIWASLP 349
 QY 324 PVAMLHTNNATLRQPFVEVLATASNAFQSLFSDVWNLRLQLSVSKVLOGTTSVLG 383
 DB 350 PKLTWKPSLLDIFVLDTQAFALPNSLDPLLEMLNLSVVGAKSDRLIGELR-LD 408
 QY 384 DVQLTVASSNGFIDTQVRLTGMVTFEKEPLDLHALLAMGIALPGVNVLEVVAPEIFV 443
 DB 409 KLLLEKHSIDIGFFSVESLQSVINYVMPTIVLPVINKLQKGFPLPAYIELFNLTLP 468
 QY 444 YGVYVVISGLPY 456
 DB 469 YCDFLLFGADVQY 481

RESULT 7
 I56246
 lipopolysaccharide binding protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
 C:Accession: I56246
 J.Su, G.B.; Freeswick, P.D.; Geller, D.A.; Wang, Q.; Shapiro, R.A.; Wan, Y.H.; Billiar, J.; Immunol. 153, 743-752, 1994
 A:Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysaccharide-binding protein
 A:Reference number: I56246; PMID:94292804; PMID:8021509
 A:Accession: I56246
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-481 <RES>
 A:Cross-references: GB:L32132; NID:g510714; PID:AAA21835.1; PID:g510715
 C:Superfamily: lipopolysaccharide-binding protein

Query Match 10.9%; Score 246.5; DB 2; Length 481;
 Best Local Similarity 24.6%; Pred. No. 6.9e-11;
 Matches 121; Conservative 79; Mismatches 210; Indels 81; Gaps 21;

QY 7 LGLLALLLPVVGASTPCTVRLNKAALSYVSEIGKAPLQALQ-VTVPHFLDWSGE---62
 DB 13 LGLLL-LSPRTQGVNPAWVRITDKGLEVAAKGLLSLQRELVKITLP---DFSGDPKI 68

QY 63 -----ALQPTRIRILNVHVPRIHLKFIAGFGVR-----LAAAFTEKVFRAPEPL-----108
 DB 69 KAVGGQYEHSLIQLSCQLRGSSLNKLPFGGLSLSDSSISVGRKWKVRRSFVKLHGS 128
 QY 109 -----ELTLPVELLADTRVTSQSSIRTPVVSISACSLFSGHAN-----EPDGSNSTSHAL 157
 DB 129 FDLVKVSTVSDLLGVDPSE-----RPTVTASCS-----NRIRDLHLVHSGNVGMLL 178
 QY 158 LVL---VQKHIAVLNKLCLSLSNLVQGV-VNVHLGTGLGNPVGSEIQIR 204
 DB 179 NLFINQIESLQKLVESKICEMIKSVTSIDLPYLQTLPTVADITDILGID-----229
 QY 205 YSMVSVPTVTSQYSLSENAVILFLG---KPIILPTDTPFVLPRHVTGEGSMATVGLSQ 262
 DB 230 YSLVAAQAKAQTLDVMEKEIFENHRSPTVTFTPT--MSLPE---DSKQVTFALSDQ 284
 QY 263 LFSALLLLQKAGALNLDIT--COLRSDNL--LNTSALGRILPEVARQPPPEPVPVVKVRL 320
 DB 285 AFNATRVYHQAGYLNFTITDEVLPPDSNIRLNTKAPRPTPLITRKYPD-MNELLGTV 343
 QY 321 GATPVAMLHTNNATLRQPFVEVLATASNAFQSLFSDVWNLRLQLSVSKVLOGTTS 380
 DB 344 VSAPLNVSPGNLSLAPQMEIEGFVILPSSARESVPRLGVTVNVFSLTFDNSKVTGMJH 403
 QY 381 VLGDVQLTVASSNGFIDTQVRLTGMVTFEKEPLDLHALLAMG---IALPGVNVLEVVA 438
 DB 404 P-EKAQVRLTESKVGMEVNLVFAFLNYLLNSLYDPVDDELAKGFPLPRRICKHDL 462
 QY 439 PEI---FVTEG 446
 DB 463 FQIKKNFLYLG 473

RESULT 8
 A35843
 lipopolysaccharide-binding protein - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1999
 C:Accession: A35843
 R.Schumann, R.R.; Leong, S.R.; Flagg, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; Science 249, 1429-1431, 1990
 A:Title: Structure and function of lipopolysaccharide binding protein.
 A:Reference number: A35843; PMID:90335281; PMID:2402637
 A:Accession: A35843
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-477 <SCH>
 A:Cross-references: GB:I35533; NID:g186965; PID:AAAS9493.1; PID:g186966
 C:Genetics:
 A:Gene: GDB:ILBP
 A:Cross-references: GDB:131571; OMIM:151990
 A:Map position: 20q11.23-20q12
 C:Superfamily: lipopolysaccharide-binding protein

Query Match 10.6%; Score 241; DB 2; Length 477;
 Best Local Similarity 23.7%; Pred. No. 1.8e-10;
 Matches 115; Conservative 93; Mismatches 219; Indels 58; Gaps 22;

QY 9 LLLALLL---PVVGASTPCTVRLNKAALSYVSEIGKAPLQ-RALQVTVPHFLDWSGEAL 64
 DB 11 LLLALLLSTPEALGANFLVARITDKGLQVAAQEGLLALQSELLRITLP---DFTGDLR 67
 QY 65 QP-----TRIRILNVH-VPRJH--LKEFIAGFGVRLLAA-----ANFTKVFRAPEPLE- 109
 DB 68 IPHVGRCGRYEHSLNIHSCELLHSGALRPVQGGSLSDSSIRVQGWKWKVRSFKKQ 127
 QY 110 -----LTPVELLADTRVTSQSSIRTPVVSISACSLFSGHAN--EPDGSNSTSHALLVL 160
 DB 128 SFDVSVKGISISVNLGLG---SESSGR-PTCYCLSCS--SDIADVEVDMVSGDWLNL 181
 QY 161 ---VQKHIAVLNKLCLSLSNLVQGV-VNVHLGTGLGNPVGSEIQIRYSWVPTVTS 216
 DB 182 HNQIESKQVLESRICEMIQKVSVDLPYLTPTVTTEIDSPADIDYSLVAPRAQA 241


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RESULT 1:
S43383
bactericidal/permeability-increasing protein - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 20-Oct-1994 #sequence_revision 15-Feb-1996 #text_change 15-Feb-1996
C:Accession: S43383
B:Qi, S.Y.; Li, Y.; O'Connor, C.D.
Biochem. J. 298, 711-718, 1994
A>Title: The region around residue 115 of human bactericidal/permeability-increasing protein
of a gene coding for the active domain and characterization of recombinant proteins.
A:Reference number: S43383
A:Accession: S43383
A:Molecule type: DNA
A:Residues: 1-250 <QIS>

Query Match 5.8%; Score 132; DB 4; Length 250;
Best Local Similarity 21.7%; Pred. No. 0.013;
Matches 50; Conservative 54; Mismatches 98; Indels 28; Gaps 10;

QY 23 PGTVRLNKAALSYSEIGKAPLQAL-QVTPPHFD-----WSGEALQPTIR 70
DQ 4 PGVVRIISQGLDYASQOQTAAQKELRIKIPDYSDFKIKHLKGHSYFMDIREFQ 63
QY 71 ILNVH---VPLRLKLF-IAGFGVRLAAANFTKVFRAPEPLETLF-VELLADTRV-TQ 124
DQ 64 LPSSQISVVPVGLKFSISNANIKISGKWKAKRFLKMGNGFPLDSTEGKSIADLKGSN 123
QY 125 SSIRTPVVISACSLFSGHANEFDGNSNSTSHA--LLVLVQKHKAVLSNKL-----CLIS 178
DQ 124 PTSGKPTITCSC---SSHINSVHVHISKVGMILQLFHKIESALENKNSQCEKVT 180
QY 179 NLVQG-VNVHLGTLGLNPGVPSQIRYSMVSVPTVTSYISLEVNALVF 227
DQ 181 NSVSSKLPQVPTLPLVMTKIDSVAGINVLVAPPATTAETLTDVQMKGEFY 230

RESULT 12
T22700
hypothetical protein F55B12.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T22700
R:Sims, M.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19602
A:Accession: T22700
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-576 <WIL>
A:Cross-references: EMBL:Z75757; PIDN:CA802126.1; GSPDB:GN03023; CESP:F55B12.5
A:Experimental source: clone F55B12
C:Genetics:
A:Gene: CESP:F55B12.5
A:Map position: 5
A:Introns: 47/1; 147/3; 178/3; 290/3; 353/2; 384/2; 427/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F55B12.5

Query Match 5.8%; Score 132; DB 2; Length 576;
Best Local Similarity 21.2%; Pred. No. 0.042;
Matches 106; Conservative 72; Mismatches 208; Indels 114; Gaps 20;

QY 24 GTVRLNKAALSYSEIGKAPLQALQVTPPHFDWSGEALQPTIRILNVHVRHLKLF 83
DQ 32 GIYRLNKAALSYSEIGKAPLQALQVTPPHFDWSGEALQPTIRILNVHVRHLKLF 83
QY 84 IAGFGVRLAAANFTKVFRAPEPLETLF-----ELLADTRVTSQIRTEV 131
DQ 90 IDCKGV-----AYNISLAFRASVAEISVTVMSVEGDTAEALRELSIESEHLFDYNGTTT 145
QY 132 YSISACSLFSGHANEFDGNSNSTSHALLVTVQKHKAVLSNKLCLISNLVQGVNVHLGTL 191
DQ 146 VNASVCNVTHSELSLVFPFGSSLSALQSEIKGQIVSALRDAVC---TTAVEA---LTFV 199

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QY 192 IGLNFPVGPES-----QIRYSMVSVPTVT--SDYISLEVNALVFLLLKGP 232
DQ 199 MAQKIPPEPNYKPEACDKNKESVAELGASLCQDVTYNGFEDSEQEGNVETTVAPTP 258
QY 233 ----IILTDPATPFVLRHVGTGEGM-----ATVGLSQQLPDSALLL--LQKAGA 276
DQ 259 DDNSTLTATEEQ---KSYWGVLDLSVNHPTFTDDEMIIGL-----DGGILFNGWKADSA 310
QY 277 LNLDTIGLRSDDNLNLSALGRLLPEVA-----RQPEPMPVVLKVLGA 322
DQ 311 QQLQILNKTRLDKRGVGI-LISEYIPNTLFHHIYWDYDNGFNKXRTTPSPDKILQ-KLSK 368
QY 323 TPVAMLHTN-NATLRLQPFVEV-----LATASNSAFQSLFSDVVVNLRLQLSVSK 372
DQ 369 AVCSKCYVEVSANLTEQPILO:DAHLGARVOLSGNVSMFHGREQ:LDHVLHANTKLVTL 428
QY 373 VKLQGTTSVLGDVQLTVASSNVGFDITDQVRLMGTVEFKPLDLHLNAL-----LA 423
DQ 429 KFTVHRSIFGDSVLTNVVDVAVDVSCIQ-----EKLILKNFSCINLKVEQKFLQ 479
QY 424 MG--IALPGVNVNLYHVAPEI 441
DQ 480 LGGPLAAPLEKLFSEVPRV 499

RESULT 13
C86183
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86183
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakan, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86183
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-488 <STO>
A:Cross-references: GB:AB005172; NID:g7211993; PIDN:AAF40464.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 5.3%; Score 120.5; DB 2; Length 488;
Best Local Similarity 18.2%; Pred. No. 0.24;
Matches 94; Conservative 105; Mismatches 205; Indels 113; Gaps 22;

QY 7 IGLILLA--LILPVVGASTPG-TVRLNKAALSYSE--IGKA-----PLQ-----RALQV 51
DQ 8 LFLLLPSFFLPSTQSTDSFTSVLSQNGLDVFNLLVKNKAIASIIPLQIPRIEKSMKI 67
QY 52 TVPHFDWSGEALQPTIRILNVHVRHLKLFAGVGRLLAA-----NFTPAVF 102
DQ 68 P---FL--GGIDVVVSMKLTIELDVASSYVK--LQETGVIVASGTTNLSNMWHYSYSTW 121
QY 103 RAP-----EPLELT:PVELLADTRVTSQIRTPVVSISACS----- 138
DQ 122 LPPIEISDQIASVQVQMEIGLSLQSD-----EGLK---LSLSCGCHVEDITIELE 174
QY 139 ----LFSGHANFDSGNSNSTSHALLVTVQKHKAVLSNKLCLISNLVQGVNVHLGTL 193
DQ 175 GGASWFIYQGVNVAFKDQIGSS-----VESTIAKLTGEGVDL-----DSFLQSLPK 220
QY 194 LNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLLLKGP-----LILPTDA 239

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Db 221 EIPVDNADLVNTFTSDPILRNSSITFEIDG-LFTKGETNQVLKSPFKKSVSLVIPCNGNS 279
QY 240 TPEVLPVRHVGTEGSMATVGLSQOLFDSALLLQKAGALNDITGQLRSDNLLNTSALGR 299
Db 280 -----KMLGISVDRAVFNAAALYNADFQGVV--DKIPESLNTARWRF 324
QY 300 LIPEVAROFFEPMPVVLKVRLGATPVAMLHTNATLRLQPFVEVLATASNAFQSLFSLD 359
Db 325 IIPQYKKYPN-QDMNLNLSLSPPLVKISEQVGVANVADLVNVLNDANQVI-PVACIS 382
QY 360 VVWNLRLQLSVKVQLQGTTSVLGQVQVLTAVSSNVGFIIDQVRLMTGTVFEKPLDLHLN 419
Db 383 LMRGSGALRVGNLNGSVS-LEDFSLKAWNSIGNLHLHLLQPIVMTVIQTVPFVYAN 441
QY 420 ALLAMGIALPFGVNLHYVAPEIFVVEGVVWISSGLFY 456
Db 442 DHLEKGFPEIMHGFTLQNAEIIICSESEITVCSDAY 478
RESULT 14
229190
hypothetical protein C55C3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29190
R:Wessne, J.; Stellyes, I.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C55C3.
A:Reference number: Z20585
A:Accession: T29190
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-606 <WQE>
A:Cross-references: EMBL:U53335; PIDN:AAA96173.1; GSPDB:GN00022; CESP:C55C3.1
A:Experimental source: strain Bristol N2; clone C55C3
C:Genetics:
A:Gene: CESP:C55C3.1
A:Map position: 4
A:Introns: 61/3; 99/2; 126/2; 161/3; 283/2; 359/2; 424/1; 463/3; 522/1; 570/1

Query Match 5.1%; Score 116; DB 2; Length 606;
Best Local Similarity 21.2%; Pred. No. 0.73;
Matches 105; Conservative 76; Mismatches 186; Indels 128; Gaps 25;
QY 13 LLLPVVGASTPGTVRLNKAALSYSVEIGKAPLQRA-----LQVTVPHFLDMSGEALQPTR 68
Db 74 LLLPDVEHILP-----SNQIIIVISKVLSRFAEHQNLSTAPNKISWT--MQNMD 124
QY 69 IRLNVHVRHLKFIAGFGVRLAANFTFKVPRAPLELTLPVELLAD--TRVTOSS 126
Db 125 IGLLG-----DLSSGVNVV-----PLNLTGQVELLAQGLTFHLESS 161
QY 127 IR-----TPVWSISACSLF-----SGHANEFDG-----SNKTSALLVL--V 161
Db 162 IEKKGNSAKVTSLSCLATRDVTWTHNGGLFGLVSVFKQGVSDNVRHMLQTIICKV 221
QY 162 QKHKAVLSNKL--CLSGINLVQGVNHLGTLGPNVGPESQIRYSNVSV-----210
Db 222 RKYIDEDANEKLAEOATSSKLADLETNALQWIS--VGGDEKSRIDISSIFDSSLASKF 278
QY 211 -----PVTSDYISLEVNALVELICK--PIILPTDA-----TPPV--LPRHVGTEG 252
Db 279 FIDFRLKEHPICQENTVELASWGISFMGQGDTPFGPVDASWPGRSPPKTNVVDVSTNKC 338
QY 253 SMATVGLSQOLFDSALLLQKAGALNDITGQLRSDNLLNTSALGR-----LIPFVARQ 307
Db 339 SMIELVSDFLPNLNLHYAVQRIKVLPRTKGVSSFLRTCEGSEFCISDLAPLAEQ 398
QY 308 FPEMPVVLKVRIGAT--PVAMLTNNA-----TLRLQPFVEVLATASNAFQSL--FSLDGV 361
Db 399 YPNS---TVELAMSATRAPVLFPSEKNGGTSVSLGLVGVVFAVNGNRQVIVVDLDVV 455
QY 362 VNLRQLSVSKVQLQGTTSVLGQVQ-----TVASSNVGFIIDQVRLMTGTVFEKPL 414

Db 456 ADARL-----SIQG-HNVSSVELRKFDLKRKTGTVDISDAEIDIALLVSQLSE---504
QY 415 LOHLNALLAMGIALP 429
Db 505 -KLLNGLLVNGMP 518
RESULT 15
A90140
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: A90140
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90140
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-974 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813136; PIDN:AAK40376.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO0011
Query Match 5.0%; Score 113; DB 2; Length 974;
Best Local Similarity 20.0%; Pred. No. 2.4;
Matches 99; Conservative 78; Mismatches 217; Indels 100; Gaps 21;
QY 13 LLLPV-VGASTPGTVRLNKAALSYSVEIGKAPLQRAQVTVPHFLDMSGEALQPTRIRI 71
Db 250 VLVPIDIGSSNQ---VSLEDWGTSPDEWVAAPGETLPLTII--YVKNIGENLLSNVMLI 304
QY 72 LNVHVRHLKFIAGFG-VRLAANFTF-----KVFRAPLELTLPVELLADTRVTOSS 125
Db 305 LQSHVP---IQFLQNYTMIGFVPAGYNYTVVANYKNVTGVYVYVITLVAIDGGFMQ 361
QY 126 SIRTIV-----VSISACSLFSGHAN-----BPDGNSNSTSHALLVQK 163
Db 362 TFEPMVYVLGVNFSASSVWGTTSPNPMVWVGPENNIPLTIIQLONGSIVTVTNATLFLQSQ 421
QY 164 HIKAVLSNKLCLSGINLVQGVNHLGTLGPNVGPESQIRY-----SNVSV 211
Db 422 YPVQFLQN--VTIGNVPAGYPIPVTVLANVNTNVTNGVYITAKWYVDGVIQVVKVP 479
QY 212 TVTSDYISLEVNALVELICKPIILPTDATPFVLPVRHVGTEGSMATVGLSQOLFDSALLL 271
Db 480 IYIESLNQSVVEGIWGSLSNFI-----VAPGNNVPLTLVKNLGENLSNVSLIL 531
QY 272 QKAGALNDITGQLRSDNLLNTSALG-----RLIPEVAROFFEPMPVVLKVRIGATP 324
Db 532 QSHYPIQF-----LQNASVGVFPAGSYNYVTVTANVPFNATPGVYI-----P 575
QY 325 VAMLTNNTATLRLQPFVEVLATASNAFQSLFSDVNVNLRQLSVSKVQLQGTTSVLGD 384
Db 576 ATLVAVGGEKENIMTVDILGYVTIQ--QSLWG-----EVTSPITVS--SGET---D 621
QY 385 VQLTVASSNVGFIIDQVRLMTGTVFEKPLDLHLNALLAMGIALPGVNVNHYVAPEIF--442
Db 622 VPLTVLLKNTGDVNLNA-TIVFQNVVEPLIFH-QATAQIGIVPAGQENYATVTVSVFPN 679
QY 443 VYEGVTVISSGLFY 456
Db 680 ATPGVYVIPATLYY 693

Search completed: June 29, 2004, 11:00:55

Job time : 23 secs

Db 6 LLALLAVISLTAASPGVKVLTDKGIEYKQIGMASIQOKLTKMKVP---DLSGTEKVP 62
 Qy 56 P-----TRIRLVHVRHLHLKFIAGFGVRLAA-----ANFTFKVPR----- 103
 Db 63 PIKVKVSLTGMIVNLGLPKSALVLPFGTGVRLAINTAFINLHGNWRVRFRIQGRS 122
 Qy 104 ---APELELTLPVELLADTRVTOSSIRTPVVISASCSLFSGHAN-BFDGNSNSTHALL- 158
 Db 123 FDLAVNGLTIT-----ADIAIKSDETGRPTVSTVNCVANVGSASIKFHGGASWLYNLF 176
 Qy 159 VLQKHKHAIVLSNKLCLISNLVGVNVHGLTGLINPVGPEPESQIRYSMVSVPTVT 218
 Db 177 SYDKALRSALQKQICPLVADITDMPHLKTNLVLAQVDAIEYISWMTSPITSKSI 236
 Qy 219 SLENAVLFLLGKPIILPTDATPVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALN 278
 Db 237 EFSIKGEFFYNIKGHQEPFPTPSLPQ---DNMLYIGVSSFTPSAGFVYNAGALS 293
 Qy 279 LDTIGQL--RSDNMLNTSALGRILPEVARQFPPEPMPVVLKVLGATPVAMLHTNNATLR 336
 Db 294 LYVTDDMIPPSSPIRLNTGTGFGVPEIATKRP-GMMKKLVKTVKEPTISLEPNVTWQ 352
 Qy 337 LQPEVEVLATASAFQSLSLDDVVLRLQLSVKVKLQCTTSVLGDVQLTVASSNVGP 396
 Db 353 ASGTVTAYAIQPNNTLSPLFVLNMEGVSQAQNVTVGKLAGAIT-LNKIENTLTGTSYVQ 411
 Qy 397 IDTDQVATLMTVPEKEPDLHLNALLAMGIALPGVNLHLYVAPEIFVYEGYVWISS 452
 Db 412 FVQGSLDNIFLWLVKVVIPKVNARLEKGFPLTIGKMNLLNTQLQVLKQYMLIGT 467

RESULT 2

Q8JFX4 PRELIMINARY; PRT; 473 AA.
 ID AC Q8JFX4
 DT 01-JUN-2003 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE LBP (LPS binding protein)/BPI (Bactericidal/permeability-increasing protein)-1.
 DE LBP/BPI-1.
 GN LBP/BPI-1.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22018144; PubMed=12033361;
 RA Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,
 RA Nakamishi T., Yokomizo Y., Soma G.;
 RT "Cloning and characterization of the homolog of mammalian
 RT lipopolysaccharide-binding protein and bactericidal permeability-
 RT increasing protein in rainbow trout Oncorhynchus mykiss.";
 RL J. Immunol. 168:5638-5644(2002).
 DR ENBL; AB042025; BAB91243.1; -
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF01273; LBP_BPI_CETP; 1.
 DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
 DR SMART; SM00328; BPI1; 1.
 DR SMART; SM00329; BPI2; 1.
 SQ SEQUENCE 473 AA; 51431 MW; 3F9DF180695CA3D7 CRC64;

Query Match 17.3%; Score 392.5; DB 13; Length 473;
 Best Local Similarity 26.9%; Pred. No. 4.2e-21;
 Matches 129; Conservative 94; Mismatches 202; Indels 55; Gaps 14;
 Qy 9 LLALLPVGASTPGTVRLNKAAALSYVSEIGKAPLQALQ-VTVPHFLDWSG-EALQP 66
 Db 7 LALLALVPFALATNPVGKVKLTKEGIEYKQIGMASIQOKLTKMKVP---DLSGTERVAP 63
 Qy 67 -----TRIRLVHVRHLHLKFIAGFGVRLAA-----ANFTFKVPR----- 103

Db 64 IGKVKYSLTGTITVNLGIPYSALALVPTDGTGISTITNAFISLHGNWKIRYLSFIKDSGSP 123
 Qy 98 TFKVFAPELELTLPVELLADT--RVTOSSIRTPVVISASCSLFSGHANFDGNSNSTH 155
 Db 124 DLEV-----DGLTWTDSITIKSDETGRPTVSSVNC-VANVGSASI-----KPHGGASWLY 172
 Qy 156 ALL-VLQKHKHAIVLSNKLCLISNLVGVNVHGLTGLINPVGPEPESQIRYSMVSVPTVT 214
 Db 173 NLFSAIDKALRSALQKQICPLVADITDMPHLKTNLVLAQVDAIEYISWMTSPITS 232
 Qy 215 SDYISLVNAVLFLLGKPIILPTDATPVLPVRHVGTEGSMATVGLSQQLFDSALLLQKA 274
 Db 233 NASIDFSLKGEFFYNIKGHQEPFPTPSLPQ---NNMLYIGMSAFTTNSAGFVYNA 289
 Qy 275 GAINLDTIGQL--RSDNMLNTSALGRILPEVARQFPPEPMPVVLKVLGATPVAMLHTNN 332
 Db 290 GALSLYITDDMIPPSSPIRLNTGTGFGVPEIATKRPFS-MMKKLVKTVKEPTIFFEPNN 348
 Qy 333 ATLRQPFVEVLATASAFQSLSLDDVVLRLQLSVKVKLQCTTSVLGDVQLTVASS 392
 Db 349 VTVQASGVTAYAIQPNNTLSPLFVLNMEGVSARLYVTVGLAGAVT-LNKIENTLT 407
 Qy 393 NVGIDTDQVATLMTVPEKEPDLHLNALLAMGIALPGVNLHLYVAPEIFVYEGYVWISS 452
 Db 408 YVQGFQVRSLDNIFLWLVKVAIPKVNARLEKGFPLSGNLLNTQLQVLKQYMLIGT 467

RESULT 3

Q804Q9 PRELIMINARY; PRT; 473 AA.
 ID AC Q804Q9
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Bactericidal permeability-increasing
 DE protein/lipopolysaccharide-binding protein precursor.
 GN BPI/LBP.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Sakai M., Kono T.;
 RT "Molecular cloning of a novel bactericidal permeability-increasing
 RT protein/lipopolysaccharide-binding protein (BPI / LBP) from common
 RT carp Cyprinus carpio L. and its expression.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AU279378; BAG56095.1; -
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF01273; LBP_BPI_CETP; 1.
 DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
 DR SMART; SM00328; BPI1; 1.
 DR SMART; SM00329; BPI2; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 473 AA; 51444 MW; A68DE9C99D8F72C7 CRC64;

Query Match 17.0%; Score 385.5; DB 13; Length 473;
 Best Local Similarity 26.7%; Pred. No. 1.4e-20;
 Matches 128; Conservative 90; Mismatches 207; Indels 55; Gaps 14;
 Qy 9 LLALLPVGASTPGTVRLNKAAALSYVSEIGKAPLQALQ-VTVPHFLDWSG-EALQP 66
 Db 7 LVLNLVSVATGNTNAGYKVKRLTKGLEYGKQIGIASIQOKLTKVPR---DISGTEKVP 63
 Qy 67 -----TRIRLVHVRHLHLKFIAGFGVRLAA-----ANFTFKVPR----- 103
 Db 64 IGKVKYSLTGTITVNLGIPYSALVLPDGTGMLSIGNAYINLHGNWRVYLRILKDSGSP 123

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QY 104 --APEPELELTPVELLADTRVTSQIRTPVWSISACSLFSGHAN-EFDGNSSTSHALL-V 159
DB 124 DLAVSELSTISTVAVMSD-----DTGHTVSMNCAATVGVNVKFGGASWLYNLFSS 177
QY 160 LVQGHKAVLSNKLCLISNLSVQGVNHLGTLGLNPNVGPESQIRYSMVSVPTVTSYIS 219
DB 178 FINKALRNALQKQICPLVADSADINPHLKTNLVLAQVDAIEYSVMGVSFVLSNTSID 237
QY 220 LEVNAVLFLGKPIILPTDAPFVLRPHVTEGSMATVGLSQQLFDSALLLQKAGALNL 279
DB 238 LGKGEFYN-GQHKPEPFSPFSLP---SODTMLYIGVSAFTNSAGFVYNRAGALSL 294
QY 280 DITGQLRSDML-----LNTSALGRLLPVARQFPPEPMPVVLKVLGATPVAHLTNN 332
DB 295 YIT-----DEMIPSGSPRLNKTGFAFIPQIKWYPCGLM-MKLIVETVKEPIVTFEPNN 348
QY 333 ATLRLQPFVEVLATASNAFOSLSLSDVVNRLQLSVSKVLOGTTSVLGCVQLTVASS 392
DB 349 MTVQASSTV-AYAIQPNSTLSPLFVLNLSVSTHYYTELKLAGNVT-LNKINMSLAKS 407
QY 393 NVGFIIDTQVRLTGMVTFEKLDDHALLAMGIALPGVNVNHLVVAPEIFVYEGVWISS 452
DB 408 YVGFQVTSLDNIFTVLKFAVPEKVNARLQEGYPLPAIGMQLVNSQLKVLKYLIGT 467

RESULT 4
O42273 PRELIMINARY; PRT; 440 AA.
AC O42273 1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Bactericidal permeability increasing protein/lipoplysaccharide
DE binding protein.
DE TENP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Brain;
RX MEDLINE=98173457; PubMed=9514522;
RA Yan R.T., Wang S.Z.;
RT "Identification and characterization of temp, a gene transiently
RT expressed before overt cell differentiation during neurogenesis.";
RL J. Neurobiol. 34:319-328(1998).
DR EMBL; AF029841; AAC14583.1; -
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR SMART; SMC0329; BP12; 1.
SQ SEQUENCE 440 AA; 47435 MW; A46C2D7F3F2686 CRC64;

Query Match 16.7%; Score 377.5; DB 13; Length 440;
Best Local Similarity 27.1%; Pred. No. 5.1e-20;
Matches 126; Conservative 82; Mismatches 216; Indels 41; Gaps 11;

QY 7 LGILLALLPVVGASTPCTVVRINKAALSVYSBIGK-----APLQALQVTVPH---FLDW 59
DB 1 MGAALLADPVPQTRAPDCGGILITPLGUSYLAUESKHAENVLRQDLMPKEPQCSLAPW 60
QY 60 SGEALQPTRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAP-BPELTLTPVELLA 118
DB 61 S-----PAGTELPAKVADLWLSVPEAGRL-----GVEELRIAPLHTVMPVRSIRA 111
QY 119 DTRVTSQIRTPVWSISACSLFSGHANFEDGNSSTSHALLVLVQKHKAVLSNKLCLIS 178
DB 112 DLHYDMGPDGNLQLTLSACRTVQAQSTREASKSSRSIL-----DKVVDVMDKLCIFY 165
QY 179 KLVGVNVHGLTGLGNPVPESQIRYSMVSVPTVTSYISLEVNAVILFLGKPIILPTD 238
DB 166 KLLIFPEQLMSLTALFPVTPNCQLQYLAALPAVFSKQGIALLSLQTTTFQVAGAVVPVPS 225
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QY 239 ATPFVLRPHVTEGSMATVGLSQQLFDSALLLQKAGALNLDTGQLRSDNLTNTSALG 298
DB 226 PVFSPMPELASTSTSHLILALSEHYFTSLYTLERAGAFNMTI-----PSMLATTALA 278
QY 299 RLIEVARQFPPEPMPVVLKVLGATPVAHLTNNATLRLQPFVEVLATASNAFOSLSL 358
DB 279 QKITQVGSLYHEDLPITLSAALRSRVLVLEGRRAALKL--FLTVHIGAGSPDFOSFLSV 336
QY 359 DV-VVNLRLQLSVSKVLOGTTSVLGVDQLTVASSNVGFIIDTQVRLTGMVTFEKLDDH 417
DB 337 SADTVRAGLQSVSDTRWISTAVIEDAELSAASNVGLVRA----ALLEELFLAPVCOQ 392
QY 418 LNA-----LLAMGIALPGVNVNHLVVAPEIFVYEGVWISSGLFYQS 458
DB 393 VPANWDEVLRGSHLPHMSHFTYTDVNVVVKDYVLVPCKLKRS 437

RESULT 5
Q7T3Q8 PRELIMINARY; PRT; 473 AA.
AC Q7T3Q8 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Bactericidal permeability increasing protein/lipoplysaccharide
DE binding protein.
DE BPI/LBP.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Stenvik J., Solstad T., Leiros I., Jorgensen T.O.;
RT "Cloning and analyses of the BPI/LBP gene of the Atlantic cod (Gadus
RT morhua L.) - Implications for the evolution of the immune system.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102629; AAM52336.1; -
SQ SEQUENCE 473 AA; 51513 MW; 9471E26BC1016E8D CRC64;

Query Match 16.7%; Score 377.5; DB 13; Length 473;
Best Local Similarity 25.8%; Pred. No. 5.6e-20;
Matches 123; Conservative 100; Mismatches 209; Indels 45; Gaps 13;

QY 9 LLLALLPVVGASTPCTVVRINKAALSVYSBIGAPLQALQ-VTVPHFLDMSG-EALQP 66
DB 7 LALLALPLALSANAGVKVLTQKGLDPGRELAVASLQKLMITIKVP---DLGKERVKP 63
QY 67 -----TRIRLNHVVRHLKFIAGFGVRLAAANF-----TFKVER----- 103
DB 64 IGKRVSVTEKRVVVKGLGPSAIGLVPCTGSLITNAFLSHGRVRYKLRFIKDRGSF 123
QY 104 --APEPELELTPVELLADTRVTSQIRTPVWSISAC-SLFGSHANEFGNSSTSHALL-V 159
DB 124 DLAIKSLSIITTSILRSD-----NMGLPAMAMASCITTLGGVSVKLGHGASWLYNLFRR 177
QY 160 LVQKHKAVLSNKLCLISNLSVQGVNHLGTLGLNPNVGPESQIRYSMVSVPTVTSYIS 219
DB 178 FIEGLOSQKQKLCPLVAESVSSMNOFLKTVKMAPVDRYAEIAYPMVSSPDISSSIG 237
QY 220 LEVNAVILFLGKPIILPTDAPFVLRPHVTEGSMATVGLSQQLFDSALLLQKAGALNL 279
DB 238 LNLKGEFYNIGNHMEPPSPAPFLPNQ--EQSMYIGLSAFTANSASFVYNKAGTSL 294
QY 280 DITGQL--RSDNLTNTSALGRLLPEVARQFPPEPMPVVLKVLGATPVAHLTNNATLRL 337
DB 295 KITDMVPRSSPIRLTNTTGVJ-PQIAKLPPGLM-MVLQLKMTYKDLPLSSFEANKVTYDA 353
QY 338 QPFVEVLATASNAFOSLSLSDVVNRLQLSVSKVLOGTTSVLGVDQLTVASSNVGFI 397
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Db 354 KSLTAVAILANTKLAPFLVNLDFSVSARVYVGNKLAGAVT-LNRIDMSLGKSYVGDF 412
 Qy 398 DTQVRLTMCVTEKPKLLDHLNALLAMGIALPGVNLHYVAPLFFVVEGYVTVSSGL 454
 Db 413 KVSLSNIFQIVLKVWVLPVTVNRLKEGFFPLPSLGKLNKNTQILKGYIMIGTDL 469

RESULT 6
 Q7T3Q9 PRELIMINARY; PRT; 473 AA.
 AC Q7T3Q9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Bactericidal permeability increasing protein/lipopolysaccharide
 DE binding protein.
 GN BPI/LBP.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Stenwik J., Solstad T., Leiros I., Jorgensen T.O.;
 RT "Cloning and analyses of the BPI/LBP gene of the Atlantic cod (Gadus
 morhua L.) - Implications for the evolution of the immune system.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY102628; AA052335; -;
 DR EMBL; AY102628; AA052335; -;
 SQ SEQUENCE 473 AA; 51485 MW; 1290836926853P8P CRC64;

Query Match 16.6%; Score 376.5; DB 13; Length 473;
 Best Local Similarity 25.8%; Pred. No. 6.7e-20;
 Matches 123; Conservative 100; Mismatches 293; Indels 45; Gaps 13;

Qy 9 LLLALLLVGASPTGTVVRLNKAALSYVSIKAPLQALQ-VTVPHFLDWSG-ELQP 66
 Db 7 LALLAL-PLALSANAGVKVLTQGLDQFGRGLAVASLQKLMITKVP---DISGKRVKP 63
 Qy 67 -----TRILNVHVRLELFAIGFVGRLLAANF-----TFKVER----- 103
 Db 64 IGKRVYSVTENRVRVKGLPSSAIGLFGTGPSLITITNALSILGRWRVKYLFKDRGSP 123
 Qy 104 --APELELTLPVELLADTRVTQSSIRTPVVSISAC-SLFSGHANEFDGNSNSTHALL-V 159
 Db 124 DLAIKLSLITTSISLSD-----NMGLPAVAMASCTITLGGVSVKLGASMLYNLFR 177
 Qy 160 LVQKHIAVLNKLCLISNLVQGVNHLGLTGLNVPVGPESQIRYSMVSVPTVTSYIS 219
 Db 178 FIEKGLQSQKQKLCPLVAESVSMNQFLKTVNVMAPVDYAEIAYPMVSSPDISSSIG 237
 Qy 220 LEVNAVFLPKGPIILPTDAPFVLRHVGEGSMATVGLSQQLFDSALLLQKAGALNL 279
 Db 238 LNLKGFYNTGNHMEPPSPAPFLPQO---EQSMVLYGLSAFTANASAFVYNAGLISL 294
 Qy 280 DITSQL--RSDNLNLT-SALGRLIPEVARQPEPMPVVLKVLGATPVMALHTNATLRL 337
 Db 295 KITDDMPRSSPIRLT-NTFGVLIPQIAKLPGLM-XVLQKMTNDPLSSIEANKVTDA 353
 Qy 338 QPFEVLATASAFQSLFSLDVLVNLRLQLSVKVQLGTTGTSVLGDVQLTVASNVGFI 397
 Db 354 KSLTAVAILANTKLAPFLVNLDFSVSARVYVGNKLAGAVT-LNRIDMSLGKSYVGDF 412
 Qy 398 DTQVRLTMCVTEKPKLLDHLNALLAMGIALPGVNLHYVAPLFFVVEGYVTVSSGL 454
 Db 413 KVSLSNIFQIVLKVWVLPVTVNRLKEGFFPLPSLGKLNKNTQILKGYIMIGTDL 469

RESULT 7
 Q8IW58 PRELIMINARY; PRT; 487 AA.
 ID Q8IW58
 AC Q8IW58;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Similar to bactericidal/permeability-increasing protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040955; AA040955.1; -;
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR01124; LBP BPI CETP.
 DR Pfam; PF01273; LBP BPI CETP; 1.
 DR Pfam; PF02886; LBP BPI CETP; 1.
 DR SMART; SM00328; BPI1; 1.
 DR SMART; SM00329; BPI2; 1.
 DR PROSITE; PS00400; LBP BPI CETP; 1.
 SQ SEQUENCE 487 AA; 53880 MW; FE709D9317E5206D CRC64;

Query Match 12.7%; Score 287; DB 4; Length 487;
 Best Local Similarity 22.6%; Pred. No. 3.6e-13;
 Matches 110; Conservative 104; Mismatches 228; Indels 44; Gaps 17;

Qy 3 WASRLGALLALLLPVGCASPTGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58
 Db 15 WAS-LNVIVLIGTAVTAANVPGVVVRSQKGLDVASQQTAAQKELKRIKIPYSDSEK 73
 Qy 59 -----WSGEALQPTRIRILNVH---VPRHLKP-IGAGFVGRLLAANFTFKVFRAP 106
 Db 74 IKHLGKHYSFYSDMDIREFQLPSSQISWVPVGLKFSISNANIKISGKWKAKRFLKWSG 133
 Qy 107 PLELTLP-VELLADTRV-TQSSIRTPVVSISACSLFSGHANEFDGNSNSTSHA--LLVLVQ 162
 Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSSC---SSHINSVHVHISKVKVGMILQLFH 190
 Qy 163 KHIAVLNKL-----CLISNLVQGVNHLGLTGLNVPVGPESQIRYSMVSVPTVTSY 217
 Db 191 KTIESALNKNQNSQCEKVNVSQKLPYQTLVPMTKIDSVAGINYLGLVAPPATTAE 250
 Qy 218 LSEVNAVFLPKGPIILPTDAPFVLP--RHVTEGSMATVGLSQQLFDSALLLQKAG 275
 Db 251 LDVQMGGEFYSENH-----HNPPFPAPPVMEFFPAHDMRVYGLSDYFNTAGLVYQEA 305
 Qy 276 ALNLDITQQL--RSDNLNLT-SALGRLIPEVARQPEPMPVVLKVLGATPVMALHTNNA 333
 Db 306 VLKMTLRDDMIKESKPLRTTKFTGLPEVAKFPN---MKIQLHVSASTPHLSVQPT 362
 Qy 334 TLRLQPFVEVLATA--SNSAFQSLFSLDVLVNLRLQLSVKVQLGTTGTSVLGDVQLTVAS 391
 Db 363 GLTYPADVQVAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELK-LORLLELKH 421
 Qy 392 SNVGIFDTQVRLTMCVTEKPKLLDHLNALLAMGIALPGVNLHYVAPLFFVVEGYVTV 451
 Db 422 SNIGFFPVELLQDLMNVIVLPILVRVNEKLGKGFPLTPARVOLYVNVLPQHQNLFLFG 481
 Qy 452 SGLFYQ 457
 Db 482 ADVVYK 487

RESULT 8
 Q8BSF3 PRELIMINARY; PRT; 486 AA.
 ID Q8BSF3
 AC Q8BSF3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Weakly similar to bactericidal/permeability-increasing protein precursor.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=15390;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Epithidymis;
RX MEDLINE=2234683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK033770; BAC28468.1; -
GO; GO:0008289; P:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP_1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 486 AA; 54351 MW; 9D8F627EA5496D62 CRC64;

Query Match 11.2%; Score 253.5; DB 11; Length 486;
Best Local Similarity 22.4%; Pred. No. 1.2e-10; Indels 73; Gaps 18;
Matches 113; Conservative 97; Mismatches 222;

QY 1 MAWA-----SRGLLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQ-RALQVTVPHFELDSGEAL 64
DB 1 MTWAPDNVKNVKSALLLALIGTALTAATDPGVAMISQKGLDFACQGVVLEKELQALS 60
QY 53 VPHELDMSG-----EALQPTRIRILNVHVRRLHKLFIAGFGVRL----- 91
DB 61 VP---DFSGVFKEIKHLGKGSYEFYSMAVDGFHPNPKIEMLPDGLRVIKDAKINKG 117
QY 92 -LAAANFTKVPRAPELELTIPVLLADTRVTOSSIRTPVVISACSLFSGHAN--EFD 148
DB 118 WMSRKNP-----LKAGNFELSGVVISITDLILGSDSGHITTI--CSNCDSHIDSVHIK 171
QY 149 GSNSTSHALLVLQKHIVKAVLSN---KLCLISNLVQGVNVHLGTLGLNFPVGPESQI 203
DB 172 IGSMLGLHRLFRHKIETSLKNIYKICKIVRDSVSKLQPYLKTLSVITRVDVTSV 231
QY 204 RYMSVPTVTSYISLVNAVFLGKPIILPTDTPVLRPHVGTGSMATVGLSQOL 263
DB 232 DYS-LAPLTTMQFLEGQLKGEFFRGRHDPFIH--PFWM-RFVPMGAYMVMCGISDYF 288
QY 264 FDEA-LLLQKAGALNDITGOLRSDN--LNTSALGRILPEVARQPE-----PM 312
DB 289 FNTVLAQQSGTLKWTGGQLLSNGRFLQNLIDFLRFLPKVAKMFPBMGVQLLISAPV 348
QY 313 PVW-KVRLGATFVAMLHTNNAFLRQPFVVLATASNSAFQSLFSDVV---VNLQLQS 369
DB 349 PVHLSIQ---PSGL--SFNPKLETAQFV---VLPNASLVFLVGLMVRKTNASLEVD 398
QY 370 VSKVKLQGTTSVLGVQVLTAVSSNVGFDITDQVRLMGTVFEKPLLDHLLNALLANGIALP 429
DB 399 AENRVLGEMKLGSRWLELKEKSFPEKVEYLEDVINYLVSTLVLPLKINERLRGFFLP 458
QY 430 GVNHLHYVAPEIFVYGVYVWISSGL 454
DB 459 LPAGIRSFHFTFPYQNFLLLEADL 483

RESULT 9
Q8TCF0 PRELIMINARY; PRT; 477 AA.
AC Q8TCF0;
D7 01-JUN-2002 (Tremblrel. 21, Created)
D7 01-JUN-2002 (Tremblrel. 21, Last sequence update)
D7 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Lipopolysaccharide binding protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Liver;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022256; AAH22256.1; -
GO; GO:0008289; P:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP_1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PSC0400; LBP_BPI_CETP; 1.
SQ SEQUENCE 477 AA; 52933 MW; 03D5E9D55A3BA6D0 CRC64;

Query Match 11.2%; Score 253; DB 4; Length 477;
Best Local Similarity 25.1%; Pred. No. 1.3e-10; Indels 72; Gaps 23;
Matches 117; Conservative 83; Mismatches 195;

QY 9 ILLALLL---PVVGASTPGTVVRLNKAALSYVSEIGKAPLQ-RALQVTVPHFELDSGEAL 64
DB 11 ILLALLLSTPEALGANPGLVARI-TKGLQYAAQEGLLALQSELLRITLP---DFTGDLR 67
QY 65 QP-----TRIRILNVH-VRRLH--LKFIAGFGVRLAA-----ANFTKVPRAPELE- 109
DB 68 IPHVGRGRYEPHSLNTHSCHELLHSLRPPVGGGLSLISDSSIRVQGRWKVRKSFKLQ 127
QY 110 -----LTLPEVLLADTRVTOSSIRTPVVISACSLFSGHAN-EFDGNSNSTSHALLVL 160
DB 128 SPDVSVKGSISVNLGLG---SESSGR-FYTVASSCS--SDIADVEDVDSGGLGWLNL 181
QY 161 ---VOKHKAVLSNKLCLISNLVQGVNVHLGTLGLNFPVGPESQIRYSMVSVPTVTS 216
DB 182 HNQIESKQKVLKRICEMIQKSVSDQLQYLQTLPTVTEIDSFADISLVEAPRATAQ 241
QY 217 YTSLEVNAPL-----ILGKPIILPTDTPVLRPHVGTGSMATVGLSQQLPDSA 267
DB 242 MLEVMFKGEIPIHNRHSPVTLAAVMSLPEE-----HNQVYFAISDYVFNCTA 289
QY 268 LLLQKAGALNDIT-GOLRSDN--LNTSALGRILPEVARQPEPMPVVLKVLGATPV 325
DB 290 SWYHEBGLNFIETDDMIIPDSNIRLTKTSRFPVRLARLYPN-MNLELQ---GSVPS 345
QY 326 A-XLHTNNATLQPFVEV--LATASNSAFQSLFSDVVVNLRLQSLSKVLQGTTSVL 382
DB 346 AELLNFSNGLSVDPVMEIDAFVLLPSSSKPEVRLSVATNVSATLTENTSKITGLKP- 404
QY 383 GQVQLTVASSNVGFDITDQVRLMGTVFEKPLLDHLLNALLANGIALP 429
DB 405 GKVKVELKESKVLGNELLEALLNYILNTFPKFNDKLAEGFPPLP 451

RESULT 10
Q95JG0 PRELIMINARY; PRT; 503 AA.
AC Q95JG0;
D7 01-DEC-2001 (Tremblrel. 19, Created)
D7 01-DEC-2001 (Tremblrel. 19, Last sequence update)
D7 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Phospholipid transfer protein.
GN PLTP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Testis;
RA Wasson D.; Lagrost L.; Bon P.;
RT "Oryctolagus cuniculus phospholipid transfer protein (PLTP) mRNA";
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.


```

DR Pfam: PF01273; LBE_BPI_CETP_1.
DR Pfam: PF02886; LBE_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS0040C; LBP_BPI_CETP; 1.
SQ SEQUENCE 503 AA; 55600 MW; 850995A71B1E8F38 CRC64;

Query Match 7.9%; Score 179.5; DB 6; Length 503;
Best Local Similarity 20.9%; Pred No. 4 Se-05;
Matches 106; Conservative 208; Mismatches 208; Indels 105; Gaps 20;

QY 8 GLLALILPVGASTPTGVRLKKAALSYVSEIGKAPLQRALQ-VTVPFLDWGEALQP 66
Db 5 GAVFLALLAGAAHEIPGCKIRVTSEALAIKVKQGLRLEQELEAITPDLRGREGHF-- 62
QY 67 TRIRILNVHPRHLKFIAGGVRLLAAANFTKVPRAPELELTLPVELL----- 117
Db 63 --YNSIDVKVTELQ---TQSEHLHFQEQELALQITNA--SLGLRFRQLLYWFFYDGY 115
QY 118 ADTRVTQSSIRTPVWSISACLSFGSHANEFDGSN-----STSHA-----LL 158
Db 116 INASAEGVSIPT-----ALQSQGPAGQMRVSNVSCLASVSRMHAAPGGTFRKVPYFELS 169
QY 159 VLVQKHKIVLKNKLC-----LSISNLVQGVNVH--LGTLLGLNPVGPESQIRYSMV 208
Db 170 TFIISGMRFLNLIQICPLVHAGMVLNLSLIDTPVRSANDELVID-----YSLL 220
QY 209 SVETVTSDXISLEVNALFLL--GKPIILPTDAPFVLPRHVHTEGSMATGLSQQLPDS 266
Db 221 KDPVWSNSYLDMFRGAFFPLAEGNWSFLNRAVEP-----QLQSEERMYVAFSEFFPDS 275
QY 267 ALLLLQKAGALNLDITC-QLRSD-DNLIINTSALGRLI---PEVARQPEPMPVVLKVRIG 321
Db 276 AMESYFRAGALKLSLVGDKVPHEDILILRATYFISVILLSPAVI-----DSPLKLEQVT 330
QY 322 ATPVAMLHTNNATLR-----LQPFVEVLATASNAFQSLFSLDVVVMRLQLS 369
Db 331 APPRCTIKPSGTTISVATVTIALLVPMPQEVQLSSVMMDARFSAKVALRGKA-LRTOLD 389
QY 370 VSKVKLGTTISVLGDVOLTVASSNVGFDITDQVTLMTGTFEKLPLDLHLLNALLAMGIALP 429
Db 390 LRKFRMTYSNDSATESLALI-----PQAPLKLTLQIGVMPMLNERTHKGVIQIP 437
QY 430 GVMNLHYVAPEIFVYEGYVWISSGLFY 456
Db 438 LPEGINFREVWVTHNAGFLTAGDLHF 464

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RESULT 12
Q8WNW7 PRELIMINARY; PRT; 496 AA.
AC Q8WNW7
DT 01-MAR-2002 {T-EMBLrel. 20, Created}
DT 01-MAR-2002 {T-EMBLrel. 20, Last sequence update}
DT 01-OCT-2003 {T-EMBLrel. 25, Last annotation update}
DE plasma phospholipid transfer protein.
GN PLTP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RZ SEQUENCE FROM N.A.
RC TISSUE=placenta;
RX MEDLINE=97396085;
RA Pussinen P.J., Oikkonen V.M., Jauhainen M., Ehnholm C.;
RT "Molecular cloning and functional expression of cDNA encoding the pig
RT plasma phospholipid transfer protein.";
RL J. Lipid Res. 38:1473-1481(1997).
EL ENBL; L78843; AAL40162.1; -
DR GC; G0:0008289; F.lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_C1P2.
DR Pfam; PF01273; LBP_BPI_C1P1; 1.

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OM nucleic - nucleic search, using sw model
Run on: June 29, 2004, 20:34:40 ; Search time 11448 Seconds
(without alignments)
6932.311 Million cell updates/sec

Title: US-10-069-034-65
Perfect score: 1831
Sequence: 1 gctcataagtagcctctg.....ttgagtgcaaaaaaaaaa 1831

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 216715:6995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
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- 12: gb.sy.*
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- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
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- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1831	100.0	1831	6	AX083523	AX083523 Sequence
2	1816.8	99.2	1820	6	AX376430	AX376430 Sequence
3	1816.8	99.2	1820	6	AX454736	AX454736 Sequence
4	1816.8	99.2	1820	6	AX491214	AX491214 Sequence
5	1816.8	99.2	1820	9	AX358723	AX358723 Homo sapi
6	1810.4	98.9	1812	6	AX280153	AX280153 Sequence
7	1810.4	98.9	1928	9	AK027068	AK027068 Homo sapi
8	1773.8	96.9	1794	6	AX166348	AX166348 Sequence
9	1772.2	96.8	1794	6	AX166346	AX166346 Sequence
10	1764.2	96.4	1842	9	BC034415	BC034415 Homo sapi
11	1375.4	75.1	1377	9	AF465765	AF465765 Homo sapi
12	1374.7	75.0	1374	6	AX166357	AX166357 Sequence
13	1372.4	75.0	1374	6	AX166356	AX166356 Sequence
14	1076.4	58.8	1533	6	AX380531	AX380531 Sequence
15	367	20.0	129502	9	HSD0726C3	AL121756 Human DNA
16	123.2	6.7	255562	2	AC095199	AC095199 Rattus no
17	123.2	6.7	298126	2	AC128629	AC128629 Rattus no
18	120.4	6.6	168210	2	AC116700	AC116700 Mus muscu
19	120.4	6.6	226251	10	AL833803	AL833803 Mouse DNA
20	107.8	5.9	1842	6	AX283507	AX283507 Sequence
21	107.8	5.9	1914	6	AX283509	AX283509 Sequence
22	107.8	5.9	2059	9	AF549190	AF549190 Homo sapi
23	107.8	5.9	2370	6	AX823158	AX823158 Sequence
24	98.2	5.4	1419	6	AX283581	AX283581 Sequence
25	97.6	5.3	1641	6	AX592783	AX592783 Sequence
26	96.8	5.3	1454	9	AF549189	AF549189 Homo sapi
27	95.2	5.2	1842	10	BC048084	BC048084 Mus muscu
28	92	5.0	1733	10	RRYA3	X60658 R.rattus RY
29	89.6	4.9	1597	5	AF029841	AF029841 Gallus ga
30	87.2	4.8	1924	6	AX166373	AX166373 Sequence
31	86.4	4.7	1897	10	RRRY2G5	X60660 R.rattus RY
32	85.6	4.7	1524	9	AF465766	AF465766 Homo sapi
33	85.6	4.7	1924	6	AX166385	AX166385 Sequence
34	79	4.3	1428	6	AX166358	AX166358 Sequence
35	79	4.3	1428	6	AX166359	AX166359 Sequence
36	70.2	3.8	1666	5	AB042025	AB042025 Oncorhync
37	69.6	3.8	125020	9	AF429315	AF429315 Homo sapi
38	67.4	3.7	1741	5	AB042026	AB042026 Oncorhync
39	66.2	3.6	1362	6	AX166389	AX166389 Sequence
40	66.2	3.6	1362	9	AF465767	AF465767 Homo sapi
41	66.2	3.6	1365	6	AX181670	AX181670 Sequence
42	66.2	3.6	1365	6	AX283325	AX283325 Sequence
43	65	3.5	125020	9	AF429315	AF429315 Homo sapi
44	61.8	3.4	7218	6	166494	I66494 Sequence 14
45	59.2	3.2	1155	6	AX166381	AX166381 Sequence

ALIGNMENTS

RESULT 1	AX083523	AX083523	1831 bp	DNA	linear	PAT 28-FEB-2001
LOCUS	AX083523	Sequence 65 from Patent WO0112662.				
DEFINITION	AX083523	Sequence 65 from Patent WO0112662.				
ACCESSION	AX083523	GI:13185333				
VERSION	AX083523.1	GI:13185333				
KEYWORDS		Homio sapiens (human)				
SOURCE		Homio sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
REFERENCE		Mammalia; Euthera; Primates; Catarrhini; Homioidae; Homo.				
AUTHORS		1 Lal, P., Yue, H., Tang, Y. T., Bandman, O., Burford, N., Aizimzai, Y.,				
		Baughn, M. R., Lu, D. A. and Patterson, C.				
TITLE		Membrane associated proteins				

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0169848-A 497 20-SEP-2001; Genentech, Inc. (US)
FEATURES	Location/Qualifiers source 1..1820 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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DB	1 GCCTTATAAGTAGCCTCTGCATCTGCCTGCGCGAGGAGGGGTACCTGGGGCT 60
QY	61 GAGAGTTTCACCTGCTCAGGAACACCTGAGCCACAGATCCTGTGGGCAGGCGCAGG 120
DB	61 GAGAGTTTCACCTGCTCAGGAACACCTGAGCCACAGATCCTGTGGGCAGGCGCAGG 120
QY	121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCCCTGCTGCTGGCACTGCTGTCGCCGTGGTGTG 180
DB	121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCCCTGCTGCTGGCACTGCTGTCGCCGTGGTGTG 180
QY	181 GTGCTCTCAGCCAGGACCGTGTCTCGACTCAACAAGGACAGCATGTGAGCTACGTGTCTG 240
DB	181 GTGCTCTCAGCCAGGACCGTGTCTCGACTCAACAAGGACAGCATGTGAGCTACGTGTCTG 240
QY	241 AAATTGGGAAGCCCTCTCCAGCGGGCCCTGCAGGTCACGTCCCTCATTTTCCTGGACT 300
DB	241 AAATTGGGAAGCCCTCTCCAGCGGGCCCTGCAGGTCACGTCCCTCATTTTCCTGGACT 300
QY	301 GGAGTGAGAGGGCGCTTCAGCCCAACAGGATTCGGATTCTGAAATGTCCATGTGCCCGCC 360
DB	301 GGAGTGAGAGGGCGCTTCAGCCCAACAGGATTCGGATTCTGAAATGTCCATGTGCCCGCC 360
QY	361 TCACCTGAAATTCATTGCTGGTTTCGAGTGGCGCTGCTGGCAGCAGCTAATTTACTT 420
DB	361 TCACCTGAAATTCATTGCTGGTTTCGAGTGGCGCTGCTGGCAGCAGCTAATTTACTT 420
QY	421 TCAAGTGCTTTTCGGCGCCAGAGCCCTGAGAGCTGAGCGTCCCTGTGGAACCTGTGGCTG 480
DB	421 TCAAGTGCTTTTCGGCGCCAGAGCCCTGAGAGCTGAGCGTCCCTGTGGAACCTGTGGCTG 480
QY	481 ACACCCGCGTSAACCCAGAGCTCCATCAGGACCCCTGTGTGTCAGCATCTCTGCCTGCTTT 540
DB	481 ACACCCGCGTSAACCCAGAGCTCCATCAGGACCCCTGTGTGTCAGCATCTCTGCCTGCTTT 540
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DB	541 TATTCTGGGCGCAGGCCAAAGAGTTTGTATGTGACGTAAACAGCACTCCACGCGCTGCTGG 600
QY	601 TCTGTGTGCAAGACACATTAAAGCTGTCTTGTAGTAAACAGCTGTGCTCTGAGCATCTCCA 660
DB	601 TCTGTGTGCAAGACACATTAAAGCTGTCTTGTAGTAAACAGCTGTGCTCTGAGCATCTCCA 660
QY	661 ACCTGTGTCAAGGCTGCTCAATGTCCACCTGGGCACTTAATTGGCTCAACCCCGTGGTCT 720
DB	661 ACCTGTGTCAAGGCTGCTCAATGTCCACCTGGGCACTTAATTGGCTCAACCCCGTGGTCT 720
QY	721 CTGAGTCCCAAGATCCGCTATTTCATGTGTCAGTGTGCCACCTGTCAACAGTCACTACATT 780


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Db 901 TCTCCAGCAGCTGTTTGAATCTGCGCTCTCTGCTGCTGAGAGGCGCGTGGCCCTCAAC 960
QY 961 TGGACATCACAGGGCAGCTGAGGTGGATGACAACTGCTGTAACACCTCTGCTGGGCC 1020
Db 961 TGGACATCACAGGGCAGCTGAGGTGGATGACAACTGCTGTAACACCTCTGCTGGGCC 1020
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Db 1021 GGCTCATCCCGAGGTGGCCCGGCTGTTCCCGAGCCCATGCTGGTGGCTCAGGTGC 1080
QY 1081 GGCTGGGTGCCACACTGTGGCCATGCTCCACAAACACCCACCTGCGGCTGGCAGC 1140
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Db 1441 CTGAGATCTTGTCTATGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
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Db 1501 GAGGACAGCAGCTGGAGGCTGAGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 TTTCAAGCCTCTGGGAACTGAGGCAAAACATACCTAGTCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 1561 TTTCAAGCCTCTGGGAACTGAGGCAAAACATACCTAGTCTGCTGCTGCTGCTGCTGCTGCT 1620
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DEFINITION Sequence 1 from Patent WO01/77148.
ACCESSION AX280153

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VERSION AX280153.1 GI:16607549
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Grell,M., Duecker,K., Hoheisel,J. and Frohme,M.
TITLE Human lipid binding protein 1
JOURNAL Patent: WO 0177148-A 1 18-OCT-2001;
MERCK PATENT GmbH (DE)
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DEFINITION AK027068
ACCESSION AK027068
VERSION AK027068.1 GI:10440095
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1
Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1928)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicd@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX166346
Sequence 1 from Patent WO0136478.
AX166346
AX166346.1 GI:14546799

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

linear

DNA

1794 bp

PAT 22-JUN-2001

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ACCESSION BC034415
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1842)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.S.,
Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
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Fahney, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalinski, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1842)
Strausberg, R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20902-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lough, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Manavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAP Plate: 51 Row: J Column: 24
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VERSION AX166357.1 GI:14546808
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AUTHORS Ballinger, D.G., Mulero, J.J., Qian, X., Wise, N.K., Haley, D.A. and
Boyle, B.J.
TITLE Methods and compositions relating to bactericidal/permeability
increasing factor-like polypeptides and polynucleotides
JOURNAL Patent: WO 0136478-A 12 25-MAY-2001;
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DEFINITION Sequence 11 from Patent WO0136478.
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VERSION AX166356.1 GI:14546807
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AUTHORS Ballinger,D.G., Mulero,J.J., Qian,X., Mize,N.K., Haley,D.A. and
Boyle,B.J.
TITLE Methods and compositions relating to bactericidal/permeability
increasing factor-like polypeptides and polymucleotides
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AUTHORS Sheppard, P.O. and Presnell, S.R.
TITLE Mammalian secreted proteins
JOURNAL Patent: WO 0202621-A 83 10-JAN-2002;
ZymoGenetics, Inc. (US)
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Db      1087 GTGCTGGGGGGA-TGTCAG-TCAAGTGGGCTCTCTCCAAAGTGGGCTTCATTGATAC 1142

RESULT 15
HSDJ726C3
LOCUS
DEFINITION
HSDJ726C3 129502 bp DNA linear PRI 13-FEB-2001
Human DNA sequence from clone RP4-726C3 on chromosome 20. Contains
the ortholog of potential ligand binding protein RYA3 (Rat), the
ortholog of potential ligand binding protein RV235 (Rat), the 5'
end of a gene similar to SPAG4 (sperm associated antibody 4), a
novel genes, a GSI pseudogene, ESTs, STSs, GSSs and a CpG island,
complete sequence.
AL121756
AL121756.14 GI:6624940
HTG; CpG island; RY265; RYA3; SPAG4.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 129502)
Collier, R.
Direct Submission
Submitted (18-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humqu@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Dec 21, 1999 this sequence version replaced gi:6469400.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em.; ENBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
RP4-726C3 is from the library RPI-4 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCVPAC2
This sequence is the entire insert of clone RP4-726C3. The true left
end of clone RP4-73023 is at 33319 in this sequence. The true
right end of clone RPI1-60H7 is at 93434 in this sequence. This
sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

```

as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

FEATURES

source

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1. .129502
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RP4-726C3"
/clone_lib="RPI-4"

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repeat_region

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257..568
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repeat_region

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596..904
/note="AluY repeat: matches 1..309 of consensus"

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gene

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complement(1300..16087)
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mRNA

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9318..9367,11754..11815,12892..12958,14267..14341,
14541..14599,15944..16087)
/gene="dj726C3.1"

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CDS

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/product="dj726C3.1.1 (Novel protein similar to SPAG4
(sperm associated antibody 4) from Rat, Isoform In)"
/note="match: ESTs: Em:AI614159 Em:AI953736 Em:AA497734
Em:AW664674 Em:AI337193 Em:BF061787 Em:AJ476737
Em:AI990192 Em:AA725516 Em:AA926974 Em:AA884824
Em:AA492755 Em:AI913795 Em:AI614179"
/evidence=not_experimental
complement(join(<1300..1378,7299..7407,8004..8038,
9318..9367,11754..11815,12892..12958,14267..14341,
14541..14599,15944..16020))
/gene="dj726C3.1"
/note="Continues in Em:AL139826 as BA60H7.1"
/codon_start=1
/evidence=not_experimental

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repeat_region

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1762..1985
/note="MIR repeat: matches 74..165 of consensus"

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repeat_region

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/note="MIR repeat: matches 2..249 of consensus"

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misc_feature

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complement(1995..2483)
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/note="match: GSS: Em:AQ761668"

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repeat_region

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2193..2609
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repeat_region

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2623..2708
/note="MIR repeat: matches 79..168 of consensus"

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repeat_region

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3006..3227
/note="MIR repeat: matches 2..256 of consensus"

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repeat_region

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3609..3803
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repeat_region

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3817..3980
/note="MIR repeat: matches 1..168 of consensus"

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repeat_region

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4215..4775
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repeat_region

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4765..4933
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repeat_region

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5379..5568
/note="HAL1 repeat: matches 360..527 of consensus"

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misc_feature

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/note="match: STS: Em:HSPF18G5"

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repeat_region

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6071..6296
/note="LIME repeat: matches 1094..1328 of consensus"

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repeat_region

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6297..6566

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/notes="AluX repeat: matches 1. .298 of consensus"
6562. .6869
/notes="LINEC repeat: matches 1328. .1594 of consensus"
6901. .7264
/notes="HAL1 repeat: matches 590. .959 of consensus"
7700. .7938
/notes="MIR repeat: matches 9. .256 of consensus"
8218. .8285
/notes="17 copies 4 mer atcc 73% conserved"
8356. .8419
/notes="16 copies 4 mer atcc 73% conserved"
9410. .9592
/notes="MIR repeat: matches 16. .202 of consensus"
9737. .10037
/notes="AluB repeat: matches 1. .291 of consensus"
10047. .10172
/notes="AluSg/x repeat: matches 180. .305 of consensus"
10174. .10416
/notes="L1 repeat: matches 3918. .4160 of consensus"
10417. .10735
/notes="AluO repeat: matches 1. .303 of consensus"
10736. .10970
/notes="L1 repeat: matches 4160. .4394 of consensus"
10993. .11282
/notes="AluSg1 repeat: matches 1. .291 of consensus"
complement(join(11533. .11815,12892. .12958,14267. .14341,
14541. .14599,15944. .>15987))
/genes="dJ726C3.1"
/product="dJ726C3.1.2 (Novel protein similar to SPAG4
(sperm associated antibody 4) from Rat, isoform 2))"
/notes="match: ESTs: Em:AI953736 Em:AI990192 Em:AI476737
Em:AA926974"
/evidence=not_experimental
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15944. .>16039))
/genes="dJ726C3.1"
/product="dJ726C3.1.3 (Novel protein similar to SPAG4
(sperm associated antibody 4) from Rat, isoform 3))"
/notes="match: ESTs: Em:AW664674 Em:AA725516 Em:BF061787
Em:AI337183"
/evidence=not_experimental
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14541. .14599,15944. .>15987))
/genes="dJ726C3.1"
/codon_start=1
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(sperm associated antibody 4) from Rat, isoform 2))"
/protein_id="CAC29360.1"
/db_xref="GI:12964591"
/db_xref="RENTREMBL:CAC29360"
/translation="GALLEDAVHNPRPPIAQRGNTSRMAEDTSPNNNDNILLPVRN
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11632. .11716
/notes="MIR repeat: matches 58. .144 of consensus"
complement(join(11658. .11815,14267. .14341,14541. .14599,
15944. .16020))
/genes="dJ726C3.1"
/codon_start=1
/evidence=not_experimental
/product="dJ726C3.1.3 (Novel protein similar to SPAG4
(sperm associated antibody 4) from Rat, isoform 3))"
/protein_id="CAC29361.1"
/db_xref="GI:12964592"
/db_xref="RENTREMBL:CAC29361"
/translation="MPRSRSRSGDGLLEDVAHNPRPPIAQRGNTSRMAEDTSPN
MNDNILLPVRNNDQALGLTQMLGVYSCARSSWRQAFCSVLVCPFLAPSPRW
RYFWALALIIGHWARTAT"
11905. .11991
/notes="L2 repeat: matches 2379. .2487 of consensus"
12235. .12248
/notes="L2 repeat: matches 2376. .2420 of consensus"

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repeat_region 12251. .12542
/notes="AluB repeat: matches 1. .300 of consensus"
repeat_region 13186. .13329
/notes="8 copies 18 mer 71% conserved"
repeat_region 13187. .13320
/notes="67 copies 2 mer tt 73% conserved"
repeat_region 13188. .13355

Query Match 20.0%; Score 367; DB 9; Length 129502;
Best local Similarity 98.7%; Pred. No. 1.3e-68;
Matches 370; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1448 CTTTGCTATGAGGGCTAGCTGGTGATATCCAGTGACTTCTACAGAGCTGAGGCAA 1507
DB 35009 CTTTGCCCTTCAGGGCTAGCTGGTGATATCCAGTGACTTCTACAGAGCTGAGGCAA 35068
QY 1508 GACCACTGGGAGGCTGAGAGTGCGCCAGCTCGCTGCTCAGGGGAAATTTCTCATTTCAAG 1567
DB 35069 GACCACTGGGAGGCTGAGAGTGCGCCAGCTCGCTGCTCAGGGGAAATTTCTCATTTCAAG 35128
QY 1568 CCACTGGGAAACTGAGGCAAAACCATATCTAGTATCATCAACCAAGCTGGACTGCTTAG 1627
DB 35129 CCACTGGGAAACTGAGGCAAAACCATATCTAGTATCATCAACCAAGCTGGACTGCTTAG 35188
QY 1628 CTGGGCTGTTTATCTTCCCTCAGTGCCCTGCTCCCTCCCTCCTCCTCTGCCCCCACC 1687
DB 35189 CTGGGCTGTTTATCTTCCCTCAGTGCCCTGCTCCCTCCCTCCTCTGCCCCCACC 35248
QY 1688 TTCTCTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1747
DB 35249 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35308
QY 1748 CAGGGGGAGGAGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1807
DB 35309 CAGGGGGAGGAGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35368
QY 1808 TCTCTTGAGCTGCAA 1822
DB 35369 TCTCTTGAGCTGCAA 35383

Search completed: June 30, 2004, 01:08:48
Job time : 11454 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OX nucleic - nucleic search, using sw model

Run on: June 25, 2004, 20:33:10 ; Search time 1059 Seconds

(without alignments)
7345.090 Million cell updates/sec

Title: US-10-069-034-65

Perfect score: 1831

Sequence: 1 gccctataaagtagccrctg.....ttgagctgcaaaaaaaaaa 1831

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	1831	4	AAF81768 Human mem
2	1816.8	99.2	1820	4	AAF81768 Human DNA
3	1816.8	99.2	1820	6	ABL88232 Human PRO
4	1816.8	99.2	1820	6	ABL95721 Human ang
5	1816.8	99.2	1820	7	ABX78776 Human PRO
6	1816.8	99.2	1820	7	ACA75748 Novel hum
7	1816.8	99.2	1820	7	ACA71228 Human sec
8	1816.8	99.2	1820	7	ACC87756 Human sec
9	1816.8	99.2	1820	7	ACC87142 Human sec
10	1816.8	99.2	1820	7	ACD04315 Human sec
11	1816.8	99.2	1820	7	ACA69646 cDNA enco
12	1816.8	99.2	1820	7	ACA90491 Novel hum
13	1816.8	99.2	1820	7	ACC89598 Human sec
14	1816.8	99.2	1820	7	ACA98389 Novel hum
15	1816.8	99.2	1820	7	ACA94031 Human sec
16	1816.8	99.2	1820	7	ACD15424 Human sec
17	1816.8	99.2	1820	7	ACD09011 Human sec
18	1816.8	99.2	1820	7	ACC96931 Human sec
19	1816.8	99.2	1820	7	ACF15652 Human sec
20	1816.8	99.2	1820	7	ACA73019 Human PRO
21	1816.8	99.2	1820	7	ACD03191 Novel hum
22	1816.8	99.2	1820	7	ACD02006 Novel hum
23	1816.8	99.2	1820	7	ACA92198 Novel hum

24	1816.8	99.2	1820	7	ACA89623	ACA89623 cDNA enco
25	1816.8	99.2	1820	7	ACA73633	ACA73633 Human sec
26	1816.8	99.2	1820	7	ACA05948	ACA05948 Human sec
27	1816.8	99.2	1820	7	ACA66782	ACA66782 cDNA enco
28	1816.8	99.2	1820	7	ACF20357	ACF20357 Human sec
29	1816.8	99.2	1820	7	ACF19743	ACF19743 Human sec
30	1816.8	99.2	1820	7	ACD22031	ACD22031 Human sec
31	1816.8	99.2	1820	7	ACF13196	ACF13196 Human sec
32	1816.8	99.2	1820	7	ACD25299	ACD25299 Human sec
33	1816.8	99.2	1820	7	ACF00348	ACF00348 Human sec
34	1816.8	99.2	1820	7	ACA72405	ACA72405 Novel hum
35	1816.8	99.2	1820	7	ACD04929	ACD04929 Novel hum
36	1816.8	99.2	1820	7	ACD18390	ACD18390 Human sec
37	1816.8	99.2	1820	7	ACD08397	ACD08397 Human sec
38	1816.8	99.2	1820	7	ACA88831	ACA88831 Novel hum
39	1816.8	99.2	1820	7	ACA70273	ACA70273 Human sec
40	1816.8	99.2	1820	7	ACD12495	ACD12495 Novel hum
41	1816.8	99.2	1820	7	ACD74410	ACD74410 Human sec
42	1816.8	99.2	1820	7	ACD16038	ACD16038 Human sec
43	1816.8	99.2	1820	7	ACD25606	ACD25606 Novel hum
44	1816.8	99.2	1820	7	ACD18083	ACD18083 Human sec
45	1816.8	99.2	1820	7	ACC88370	ACC88370 Human sec

ALIGNMENTS

RESULT 1

AAF81768

ID AAF81768 standard; cDNA; 1831 BP.

XX AC AAF81768;

XX DT 12-JUN-2001 (first entry)

XX DE Human membrane associated protein MEMAP-28 encoding cDNA.

XX KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;

XX KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrhetic;

XX KW antiarteriosclerotic; gene therapy; cell proliferative disorder;

XX KW autoimmune disorder; inflammatory disorder; neurological disorder;

XX KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;

XX KW epilepsy; diarrhoea; ss.

XX OS Homo sapiens.

XX PN WO200112662-A2.

XX PD 22-FEB-2001.

XX PF 14-AUG-2000; 2000WO-US022315.

XX PR 17-AUG-1999; 99US-0149641P.

XX PR 09-NOV-1999; 99US-0164203P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;

XX PI Baughn MR, Lu DM, Patterson C;

XX DR WPI; 2001-168860/17.

XX DR P-PSDB; AAB74722.

XX PT Isolated polypeptide with a human membrane associated protein sequence is

XX PT useful for the diagnosis, prevention and treatment of cell proliferative,

XX PT autoimmune/inflammatory, neurological and gastrointestinal disorders.

XX PS Claim 5; Page 167; 173pp; English.

XX CC AAF81741 to AAF81777 encode the human membrane associated proteins

XX CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,

XX CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrhetic and

XX CC antiarteriosclerotic activities, which can be used in gene therapy.

D5 361 TCCACCTGAATTCATGCTGGTTTCGGAGTGGCGCTGCTGGCAGCAGCTAATTTACTT 420
QY 421 TCAAGGTTCTTTGGGCCCCCAGAGCCCTTGGAGCTGACGCTGCTCTGGAACCTGCTGGGTG 480
D5 421 TCAAGGTTCTTTGGGCCCCCAGAGCCCTTGGAGCTGACGCTGCTCTGGAACCTGCTGGGTG 480
QY 481 ACACCGGCTGACCGAGCTGCTATCAGGACCCCTGCTGGTGAAGCTCTGCTGCTCTT 540
D5 481 ACACCGGCTGACCGAGCTGCTATCAGGACCCCTGCTGGTGAAGCTCTGCTGCTCTT 540
QY 541 TATTCCTGGGCGACGCCAAGCTTTGATGTCAGTAACAGCAGCTCCCAAGCGCTGCTGG 600
D5 541 TATTCCTGGGCGACGCCAAGCTTTGATGTCAGTAACAGCAGCTCCCAAGCGCTGCTGG 600
QY 601 TCTGGTGCAGAGCACATTAAGCTGCTTGAAGTAACAGCTGCTGAGCATCTTCCA 660
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QY 841 CCACCCCTTTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
D5 841 CCACCCCTTTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 TCTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
D5 901 TCTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TGGACATCACAGGCGAGCTGAGTGGATGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
D5 961 TGGACATCACAGGCGAGCTGAGTGGATGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GGCTCATCCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
D5 1021 GGCTCATCCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 GGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
D5 1081 GGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 CCTTGGTGGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
D5 1141 CCTTGGTGGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 ATGTGGTGGTGAATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
D5 1201 ATGTGGTGGTGAATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 CGTCTGCT 1320
D5 1261 CGTCTGCT 1320
QY 1321 CAGATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
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QY 1441 CTGAGATCTTGTCTATGAGGGCTACCTGGTATCCAGTGGACTCTTCTACAGAGCT 1500
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QY 1501 GAGGCAAGACCACTGGAGGCTGAGAGTGGSCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
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D5 1681 CTTTCCCTTCT 1740
QY 1741 CCCACCCAGGCGGAGCAGACTGCTCTCTCAGGCTGATAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
D5 1741 CCCACCCAGGCGGAGCAGACTGCTCTCTCAGGCTGATAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 AACCACTTCTCTGAGCTGC 1820
D5 1801 AACCACTTCTCTGAGCTGC 1820

RESULT 5
ABX78776
ID ABX78776 standard; cDNA; 1820 BP.
AC ABX78776;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polynucleotide #249.
XX
KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ABEFT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 21-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 17-DEC-1997; 97US-0069425P.
PR 18-DEC-1997; 97US-0069870P.
PR 10-MAR-1998; 97US-0068017P.
PR 11-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 20-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.


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PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match          99.2%; Score 1816.8; DB 7; Length 1820;
Best local similarity 99.9%; Pred. No. 0;
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTAAAGTAGCTCTGCACTGCTGCTGGGAGAGAGGCTACCTGGGCT 60
DB 1 GCCTTAAAGTAGCTCTGCACTGCTGCTGGGAGAGAGGCTACCTGGGCT 60
QY 61 GAGAGTTCACCTGTCTCAGGAACACCTGAGCCACAGATCCTGTGGGAGGCGGAGG 120
DB 61 GAGAGTTCACCTGTCTCAGGAACACCTGAGCCACAGATCCTGTGGGAGGCGGAGG 120
QY 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTGCTGGGCTG 180
DB 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTGCTGGGCTG 180
QY 181 GTGCTCCAGCCAGGACCGTGTGCTGGCTCAACAAGGAGGAGCTAGCTAGCTG 240
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QY 241 AATTTGGGAAGGCCCTCTCAGGGGCCCTGAGGTCAGTCCCTCATTTCTGGACT 300
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DB 361 TCCACCTGAAATTCATTTGCTGGTTTGGAGTGGGCTGTGGGAGGAGCTAAATTTACT 420
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DB 421 TCAAGTCTTTTGGCGCCCGAGAGCTCCATCAGGACCCCTGTGCTCAGCATCTCTG 480
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RESULT 6

ACA75748

ID ACA75748 standard; cdNA; 1820 BP.

XX ACA75748;

XX ACA75748;

DT 07-JUL-2003 (first entry)

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XX DE Novel human secreted and transmembrane protein PRO5776 cDNA.
XX XX Human; secreted and transmembrane protein; PRO; gene therapy;
XX KW tumour necrosis factor-alpha release; TNF-alpha release;
KW KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX XX Homo sapiens.
XX XX
XX PN US2003032127-A1.
XX XX -3-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
XX 18-SEP-1997; 97US-0059263P.
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RESULT 8

ACC87756
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XX
DT 05-AUG-2003 (first entry)
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Human; PRO; secreted protein; transmembrane protein;
XX
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX
chondrocyte; proliferation; differentiation; cartilage disorder;
XX
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX
liver; drug screening; transgenic animal; genetic analysis;
XX
antiarthritic; vulnery; gene therapy; gene; ss.
XX
Homo sapiens.
XX
US2003027278-A1.
XX
06-FEB-2003.
XX
21-JUN-2002; 2002US-00176987.
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Qy	421	TCAGGTCTTTCCGCCCCCAAGCCCTGCAGCTGACGCTGCCCTGTGGAACTGCTGGCTG	480
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Qy	961	TGAGCATCAGAGGCAGCTGAGTCCGATGACAACTGTGCTGAACACCTGTGCTCTGGGCC	1020
Db	961	TGAGCATCAGAGGCAGCTGAGTCCGATGACAACTGTGCTGAACACCTGTGCTCTGGGCC	1020
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Db	1261	CGTCTGTGCTGGGGGATGTCACGCTCAQSGTGGCCCTCCTCCAAAGTGGGCTTCATTTGATA	1320
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Qy	1441	CTGAGATCTTTGTCTATGAGGGCTACGTGGTGTATTCAGTGGACTCTTCTTACCAGAGCT	1500
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Qy	1501	GAGGCAAGACCACTGGGAGGCCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCA	1560
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KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; gene therapy; gene; ss.		
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XX	US2003036159-A1.		
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ID ACA69646 standard; cDNA; 1820 BP.

XX AC ACA69646;

XX DT 27-JUN-2003 (first entry)

XX DE cDNA encoding human PRO polypeptide #249.

XX KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX KW chromosome mapping; gene mapping; cytostatic; gene therapy; gene; ss.

XX OS Homo sapiens.

XX PN US2003032113-A1.

XX PD 13-FEB-2003.

XX PF 20-JUN-2002; 2002US-00176911.

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DB	1261	CGTCTGTGCTGGGGATGTCCAGCTCAAGTGGGCTCTCTCCAAAGTGGCTTCATTGATA	1320
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QY	1441	CTGAGATCTTTGTCTATGAGGGCTACGTGTGATATCCAGTGGAGCTCTTCTACAGAGCT	1500
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DB	1561	TTTCAAGCCACTGGGGAACCTGAGGCAAAACCTAGTACTTACTATCAACCAAGCTGGAC	1620
QY	1621	TGCTAGCTGGGCTGTATTATCTTCCCTGAGTGGCTGGGCTCTCCCTCCCTCACTCTGCG	1680
DB	1621	TGCTAGCTGGGCTGTATTATCTTCCCTGAGTGGCTGGGCTCTCCCTCCCTCACTCTGCG	1680
QY	1681	CTTTCCCT	1740
DB	1681	CTTTCCCT	1740
QY	1741	CCACCCCGAGGGGAGCAGACTGCTCCAGCTGTATAGACCTGCGCTCTTGCATTA	1800
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ACC89598
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XX ACC89598;

XX 11-AUG-2003 (first entry)

XX Human secreted polypeptide PRO5776-encoding cDNA, SEQ ID NO:497.

DE Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.

OS Homo sapiens.

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Best Local Similarity 99.9%; Pred. No. 0;
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QY 181 GTGCTTCCAGCCAGGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 361 TCCACCTGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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QY 421 TCAAGGCTCTTTCCGCGCCCAAGAGCCCTGGAGCTGAGCCTGCTGCTGCTGCTGCTGCTG 480
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RESULT 14	
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DT	25-JUL-2003 (first entry)
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KW	Human; secreted and transmembrane protein; PRC; transgenic animal;
KW	knockout; chromosome identification; tissue typing; tumour;
KW	chondrocyte proliferation; chondrocyte differentiation;
KW	tumor necrosis factor-alpha release stimulator; gene; ss.
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OS	Homo sapiens.

PN US2003036144-A1.

PD 20-FEB-2003.

01-JUL-2002: 2002US-00187601

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PR 18-SEP-1997: 93US-0059266P-
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Best Local Similarity 99.9%; Pred. No. 0;		
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Query Match 99.2%; Score 1816.8; DB 7; Length 1820;
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ALIGNMENTS

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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pZgpt-F15
US-08-232-463-14

Query Match

3.4%; Score 61.8; DB 1; Length 7218;

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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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; Sequence 8422, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 8422

; LENGTH: 438

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8422

Query Match 2.5%; Score 46; DB 4; Length 438;

Best Local Similarity 61.9%; Pred. No. 0.019;

Matches 73; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1630 GGGCTGTTTTATCTTCCTCGATGCTGGGTCTCCCTCCCTCACTTCGCGCTTTCCTT 1689

DB 169 GGGGGGGCTTCTCTCCCTCCCTCTCTCCCTCACTTCGCGCTTTCCTTTCCTTCCCTC 228

QY 1690 CTTCT 1747

DB 229 CCTCCCGCCCGCCCGCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 286

RESULT 7

US-09-252-991A-8385

; Sequence 8385, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 8385

; LENGTH: 474

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8385

Query Match 2.5%; Score 46; DB 4; Length 474;

Best Local Similarity 61.9%; Pred. No. 0.019;

360	CAACATGATCTTCGTCTCGCCTTCGCCCTCGGTACCGCCCGCGCCTTCGAAATGCCGAC	415
788	AGTCAATGCTGTCTCTTCCTCTGTGGCAAGCCATCATCTGCCACGAGATGCCACCCC	847
420	CACCAGGCGCTGCTGCCGAACTTGATACCGCGCGGCTGTTCGCGCGCGCTGCGCCG	479
848	TTTTGTGTGCCAAGGCHTGTGGTATCCGAGGGCTCCATGGCCACCGTGGGCTCTCCCA	907
480	TTCCGGCTTCGGCGATACAGCGCGACCAATCCGCGCCGCGCCTCGCGGCGCTGCTCTA	539
908	GCAGCTGTTTGACTTCGCGCTCTCTGCTGTCAGAAAGCGCGTGCCTCAACTGGACAT	967
540	TGGGTTCCGTGCTCTCTGGTCTACGTGCGACCGGACTCTCTAGCTCTCGCTGCGT	599
968	CACAGGCGAGCTGAGTCCGATGACAACTGCTGAACACTCTGCTCTGGCGCGGCTCAT	1027
600	CCTGACGCTCAGCCTGCGGTACGCAACACAGCGCTCAACCCAGGCGAAGGCCACCCCTCGA	659
1028	CCGGAGGTTGGCGCGCAGTTTCCGAGCCCATGCTGTGTGCTCAAGGTGCGGCTGG	1087
660	CTCGCTCTCGCGCGACCCGTTTCACTCGCAGCGCAGCCGGACATCTTCGGGCGAATCTC	719
1088	TGCCACACCTGTGGCCATGCTCACACAAACAAACGCCACCTCTCGGCTCGAGCCCTTCGT	1147
720	CCTCGACCTGTTTCGCGCTGCTCTCTCGCGCGGCCCAACCGCCCTGCTCCGCGTTCGCCAA	779
1148	GGAGGTCCTGGCCACAGCCTCC	1169
780	GGACATCCTGCTCAGCGGCC	801

RESULT 10
US-09-252-991A-14171
; Sequence 1417, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Yarc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; CURRENT APPLICATION NUMBER: US 60/374,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/394,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14171
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14171

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; PRIOR APPLICATION NUMBER: US 60/394,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14171
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14171

Query Match                2.5%;   Score 45.2;   DB 4;   Length 1266;
Best Local Similarity      43.9%;   Pred. No. 0.047;
Matches 194; Conservative 0; Mismatches 248; Indels 0; Gaps 0;

QY      728 CCAGATCCGCTATTCATGGTCAGGTGCGCCACTGTACACAGTGACTACATTTCCCTGGA 787
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      397 CAACATGATCTTCGTCTCGCTCTCGCCCTCGGTACCGCGCGGCCCTTGAATGCGCAC 456

QY      788 AGTCAATGCTGTTCTCTTCTCTGTGGCAAGCCCATCATCTGCCACGGATGCCACCCC 847
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      457 CACCACGGCGTCTGTGCCGAACCTGGTACCGCGCGGCTGTTCCCGCGCGGTGGCCGC 516

QY      848 TTTTGTGTGCCAAGCATGTGGTATCGAGGGCTCCATGGGCCACCGTGGGCTCTCCCA 907
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      517 TTTCGGCTTCGGCGATCGAGCGGCGACCATTCGCGCCCGGCCCTCGCGGGCTGCTCTA 576

QY      908 GCAGCTGTGTGACTCTGGCTCTCTGCTGTGCAGAAAGCCGGTGGCCCTCAA CTTGCACAT 967
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      577 TGC GTTTCGGTGCCTCTCTGGTCTACGTGCCGACCGCGACTCTCTACGTCTCTCGGTGGCT 636

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D β	517	TTTCGGCTCGGGGATGCAGCGGGACCATTCGCGCCCGGCCCTCGCGGGCTGCTCTA	576
Q γ	908	GCAGCTGTGTGACTCTGCGCTCTCTGTCGAGAAAGCCGGGTGCCCTCAA	967
D δ	577	TGCGTTGGGTGCTCTGGGTCTAGCTGCCAGCCGCACTCTCTACGTCTCTCGCGTGGCT	636

[illegible]

1777 GTATAGACCTGCCCTCTTGCA 1798

D'b 86 SYNYSYNYSYNYSYNYSYNY 65

Search completed: June 30, 2004, 03:10:25
Job time : 162 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1831	100.0	1831	9	US-09-965-529-65	Sequence 65, App1	
2	1831	100.0	1831	10	US-09-969-680A-65	Sequence 65, App1	
3	1816.8	99.2	1820	13	US-10-206-915-497	Sequence 497, App1	
4	1816.8	99.2	1820	13	US-10-199-670-497	Sequence 497, App1	
5	1816.8	99.2	1820	13	US-10-201-858-497	Sequence 497, App1	
6	1816.8	99.2	1820	13	US-10-091-056-321	Sequence 321, App1	
7	1816.8	99.2	1820	13	US-10-085-890-497	Sequence 497, App1	
8	1816.8	99.2	1820	13	US-10-208-024-497	Sequence 497, App1	
9	1816.8	99.2	1820	13	US-10-201-853-497	Sequence 497, App1	
10	1816.8	99.2	1820	13	US-10-174-581-497	Sequence 497, App1	
11	1816.8	99.2	1820	13	US-10-176-483-497	Sequence 497, App1	
12	1816.8	99.2	1820	13	US-10-176-749-497	Sequence 497, App1	
13	1816.8	99.2	1820	13	US-10-176-914-497	Sequence 497, App1	
14	1816.8	99.2	1820	13	US-10-176-915-497	Sequence 497, App1	

1 GCCTATATAAGTAGCCTCTGCATCTGCCTCGCTCGGCGAGAGGGCTACCTCGGGCT 60
61 GAGGCTTCACTGCTCTCAGGAACCACTCTCAGCCACAGATCTGTGGGCGAGGGCAGGG 120
61 GAGGCTTCACTGCTCTCAGGAACCACTCTCAGCCACAGATCTGTGGGCGAGGGCAGGG 120
121 CAGCCATGGCTTGGCAAGTAGGCTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
121 CAGCCATGGCTTGGCAAGTAGGCTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
181 GTCCTTCAAGCAGGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
181 GTCCTTCAAGCAGGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
241 AATCTGGGAAGCCCTCTCAGGCGGCTCTCAGGCTCACTGCTGCTGCTGCTGCTGCTGCT 300
241 AATCTGGGAAGCCCTCTCAGGCGGCTCTCAGGCTCACTGCTGCTGCTGCTGCTGCTGCT 300
301 GGAGTGGAGAGCGCTTCAAGCCACAGGATCCGATTCGGAATTCGATTCGATTCGATTCG 360
301 GGAGTGGAGAGCGCTTCAAGCCACAGGATCCGATTCGGAATTCGATTCGATTCGATTCG 360
361 TCCACTGAAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 TCCACTGAAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 TCAAGGCTTTTCCGCCCCAGAGCCCTGAGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 480
421 TCAAGGCTTTTCCGCCCCAGAGCCCTGAGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 480
481 ACACCCGGTGACCCAGAGCTCCATCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 ACACCCGGTGACCCAGAGCTCCATCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
541 TATCTCGGCGCACCCAGAGCTTGTGAGTGAAGCTGCTGAGTGAAGCTGCTGAGTGAAGCT 600
541 TATCTCGGCGCACCCAGAGCTTGTGAGTGAAGCTGCTGAGTGAAGCTGCTGAGTGAAGCT 600
601 TCCTGGTGAGAGCACATTAAGCTGCTTCAAGTAAAGCTGCTGCTGCTGCTGCTGCTGCTG 660
601 TCCTGGTGAGAGCACATTAAGCTGCTTCAAGTAAAGCTGCTGCTGCTGCTGCTGCTGCTG 660
661 ACCTGGTGAGAGGTGCAATGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
661 ACCTGGTGAGAGGTGCAATGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
721 CTGAGTCCAGATCCGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 CTGAGTCCAGATCCGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 CCCTGGAAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
781 CCCTGGAAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
841 CCACCCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
841 CCACCCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
901 TCTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901 TCTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
961 TGGACATCAGGGCAGCTGAGTGGATGCAACCTGCTGAGCAGCTGCTGCTGCTGCTGCTGCT 1020
961 TGGACATCAGGGCAGCTGAGTGGATGCAACCTGCTGAGCAGCTGCTGCTGCTGCTGCTGCT 1020
1021 GSCCTATCCGAGAGTGGCCCGCAGTTCCGAGCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1021 GSCCTATCCGAGAGTGGCCCGCAGTTCCGAGCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1081 GSCCTGGTGCCACACTGCTGGCCATGCTCCACACAAACCCAGCTGCTGCTGCTGCTGCTG 1140
1081 GSCCTGGTGCCACACTGCTGGCCATGCTCCACACAAACCCAGCTGCTGCTGCTGCTGCTG 1140

1141 CTTCTGCTGAGGCTCTGCGCCACAGAGCTTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTG 1200
1141 CTTCTGCTGAGGCTCTGCGCCACAGAGCTTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTG 1200
1201 ATGCTGCTGAGTGAACCTTGAGACTTCCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
1201 ATGCTGCTGAGTGAACCTTGAGACTTCCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
1261 CTTCTGCTGCTGCGGATGCTGAGCTTCCAGCTTCCAACTCGGCTTTCCAGTCCCTCTTCT 1320
1261 CTTCTGCTGCTGCGGATGCTGAGCTTCCAGCTTCCAACTCGGCTTTCCAGTCCCTCTTCT 1320
1321 CAGATCAGTGGCGCACACTGATGGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1321 CAGATCAGTGGCGCACACTGATGGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1381 ATGCTCTCTGCTGCGGATGCTGAGCTTCCAGCTTCCAACTCGGCTTTCCAGTCCCTCTT 1440
1381 ATGCTCTCTGCTGCGGATGCTGAGCTTCCAGCTTCCAACTCGGCTTTCCAGTCCCTCTT 1440
1441 CTGAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1441 CTGAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1501 GAGGCAAGACCACTGCGGCGCTGAGAGTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1501 GAGGCAAGACCACTGCGGCGCTGAGAGTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1561 TTTCAAGCCACTGCGGCGGCTGAGGCAAACTGAGTGGGCGGCTGCTGCTGCTGCTGCTGCT 1620
1561 TTTCAAGCCACTGCGGCGGCTGAGGCAAACTGAGTGGGCGGCTGCTGCTGCTGCTGCTGCT 1620
1621 TGCCTAGCTGGGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1621 TGCCTAGCTGGGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1681 CTTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1681 CTTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1741 CCGACCCAGAGGGGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
1741 CCGACCCAGAGGGGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
1801 AACCACTTCTCTTGAAGCTGCAAAAAA 1831
1801 AACCACTTCTCTTGAAGCTGCAAAAAA 1831

RESULT 2

US-09-969-680A-65

; Sequence 65, Application US/09969680A

; Publication No. US20030124649A1

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti; YUE, Henry

; APPLICANT: TANG, Y. Tom; BANDMAN, Olga

; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.; LU, Dyoung Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PP-0731-1 USA

; CURRENT APPLICATION NUMBER: US/09/969,680A

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US00/22315

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/149,641

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/164,203

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 65

1021	DB	GGCTATCCCGAGGCTGGCCGCGCAGTTTCCCGAGGCCAATGCTCTGGTGTCAAGCTGC	1080
1081	QY	GGCTGGGTGCCACACCTCTGTGCCATGTCTCACACAAAACAGCCACCTCTGGCTGCAGC	1140
1081	DB	GGCTGGGTGCCACACCTCTGTGCCATGTCTCACACAAAACAGCCACCTCTGGCTGCAGC	1140
1141	QY	CTTTGGTGGAGGTCTCTGGCCACAGCTCCAACTGGGCTTTCAGTTCCTCTTCTCCCTGG	1200
1141	DB	CTTTGGTGGAGGTCTCTGGCCACAGCTCCAACTGGGCTTTCAGTTCCTCTTCTCCCTGG	1200
1201	QY	ATGTGTAAGTGAATCTGAGACTCCAGCTCTCTGTGTCCAAAGTGAAGCTTCAGGGACCA	1260
1201	DB	ATGTGTAAGTGAATCTGAGACTCCAGCTCTCTGTGTCCAAAGTGAAGCTTCAGGGACCA	1260
1261	QY	CGTCTGTCTGGGGATGTCCAGCTCACGGTGGCCCTCTCTCAAGCTGGGCTTCATTGATA	1320
1261	DB	CGTCTGTCTGGGGATGTCCAGCTCACGGTGGCCCTCTCTCAAGCTGGGCTTCATTGATA	1320
1321	QY	CAGATCAGGTTGGCCACACTGATGGGACCGTTTTTGAGAGCCCTGTCTGGACATCTCA	1380
1321	DB	CAGATCAGGTTGGCCACACTGATGGGACCGTTTTTGAGAGCCCTGTCTGGACATCTCA	1380
1381	QY	ATGCTCTCTTGGGCATCGGGAATTCGCCCTCCCTGGTGCTGGTCAACCTCCACTATGTGCCCC	1440
1381	DB	ATGCTCTCTTGGGCATCGGGAATTCGCCCTCCCTGGTGCTGGTCAACCTCCACTATGTGCCCC	1440
1441	QY	CTGAGATCTTTGTCTATGAGGGCTACGTGTGTATATCCAGTGGACTCTTCTACCAAGCT	1500
1441	DB	CTGAGATCTTTGTCTATGAGGGCTACGTGTGTATATCCAGTGGACTCTTCTACCAAGCT	1500
1501	QY	GAGGCAGACCACTGGGAGCCTTGAGAGTGGGCCAGCTCGCTGCTCAGGGAATTTCTCA	1560
1501	DB	GAGGCAGACCACTGGGAGCCTTGAGAGTGGGCCAGCTCGCTGCTCAGGGAATTTCTCA	1560
1561	QY	TTTCAAGCCACTGGGAAAATGAGGCAAAACCATACTTAGTCAATCAACCAAGCTGGAC	1620
1561	DB	TTTCAAGCCACTGGGAAAATGAGGCAAAACCATACTTAGTCAATCAACCAAGCTGGAC	1620
1621	QY	TGCTTAGCTGGGCTGTTTATCTTCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCC	1680
1621	DB	TGCTTAGCTGGGCTGTTTATCTTCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCC	1680
1681	QY	CTTTCCCTTCCTCCTCTCTCTCTCTCCCTCTTCCTCATCTCCCGCTCTCTCTCTCCG	1740
1681	DB	CTTTCCCTTCCTCCTCTCTCTCTCTCTCTCTTCCTCATCTCCCGCTCTCTCTCTCCG	1740
1741	QY	CCACCCCCGAGGGGAGCAGACTGCTCTCCAGGCTGTATAGACCTGCCCTCTTTCATTTA	1800
1741	DB	CCACCCCCGAGGGGAGCAGACTGCTCTCTCCAGGCTGTATAGACCTGCCCTCTTTCATTTA	1800
1801	QY	AACAACTCTCTTGAGCTGC	1820
1801	DB	AACAACTCTCTTGAGCTGC	1820

RESULT 5

US-10-201-858-497

US-10-201-838-437
; Sequence 497, Application US/10237858

; publication No. US29340038337A1

; GENERAL INFORMATION;

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C454
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612

Query Match	99.2%	Score 1816.8	DB 13	Length 1820
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Best Local Similarity 99.9%; Pred. No. 0; Score 1818.8

Best local similarity 55.5%, P.I.D. NO. 0;
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	GCCTTTAAAGTAGCCTCTGCATCTGCTGCTCGGGCAGAGGAGGCTACCCCTGGGAGCT	60
Db	1	GCCTTTAAAGTAGCCTCTGCATCTGCTGCTCGGGCAGAGGAGGCTACCCCTGGGAGCT	60
QY	61	GAGAGTTCACCTGTCTCAGGAACCACTGTAGCCACACAGATCCCTGTGGGCGAGCGGCCAGGG	120
Db	61	GAGAGTTCACCTGTCTCAGGAACCACTGTAGCCACACAGATCCCTGTGGGCGAGCGGCCAGGG	120
QY	121	CAGCCATGCTTTGGCAAGTAGGCTGGGCCCTGCTGCTGGCACTGCTGCTGCTGCCCGTGGTCG	180
Db	121	CAGCCATGCTTTGGCAAGTAGGCTGGGCCCTGCTGCTGGCACTGCTGCTGCTGCCCGTGGTCG	180
QY	181	GTGGCTTCCACGCCGAGCACCGTGGTCCGACTCAACAGGGCAGGATTTGAGCTAGTGTCTG	240
Db	181	GTGGCTTCCACGCCGAGCACCGTGGTCCGACTCAACAGGGCAGGATTTGAGCTAGTGTCTG	240
QY	241	AAATTTGGAAAGCCCCCTCTCCAGCGGGGCCCTGCGAGGTCACTGTCCCTCATTTCTCTGGACT	300
Db	241	AAATTTGGAAAGCCCCCTCTCCAGCGGGGCCCTGCGAGGTCACTGTCCCTCATTTCTCTGGACT	300
QY	301	GGAGTGGAGAGGCGCTTCAGGCCACGAGATTCGGATTCGATGTCCATGTGCCCGCCGCGC	360
Db	301	GGAGTGGAGAGGCGCTTCAGGCCACGAGATTCGGATTCGATGTCCATGTGCCCGCCGCGC	360
QY	361	TCCACTCGAAATTCATTGTCTGTTTTGGAGTGGCGCTGCTGGCGAGCAGCTAAATTTTACTTT	420
Db	361	TCCACTCGAAATTCATTGTCTGTTTTGGAGTGGCGCTGCTGGCGAGCAGCTAAATTTTACTTT	420
QY	421	TCAAGTCTTTTCGCGCCCGAGAGCCCTCGGAGCTGACGCTGCTGTGGAACTGCTGGGCTG	480
Db	421	TCAAGTCTTTTCGCGCCCGAGAGCCCTCGGAGCTGACGCTGCTGTGGAACTGCTGGGCTG	480
QY	481	ACACCGGCTGACCCAGAGTTCATCAGGACCCCTGTGCTGATCAGCATCTCTGCTGCTCTTT	540
Db	481	ACACCGGCTGACCCAGAGTTCATCAGGACCCCTGTGCTGATCAGCATCTCTGCTGCTCTTT	540
QY	541	TATTTCTCGGGCCAGCCAAACGAGTTTGTGGCAGTAACAGCACTCCCAAGCGGCTGCTGG	600


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; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00500
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 321
; LENGTH: 1820
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-081-056-321
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Query Match      98.2%; Score 1816.8; DB 13; Length 1820;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      - GCCTTATAAGTACCTCTGCATCTGCTCGCTCGGSCAGAGAGGGCTACCCCTGGGCT 60
DB      1 GCCTTATAAGTACCTCTGCATCTGCTCGCTCGGSCAGAGAGGGCTACCCCTGGGCT 60

QY      61 GAGAGTTCACCTCTCTCAGGAACCACTGAGCCCAACAGATCTCTGTGGGAGCGGCCAGGG 120
DB      61 GAGAGTTCACCTCTCTCAGGAACCACTGAGCCCAACAGATCTCTGTGGGAGCGGCCAGGG 120

QY      121 CAGCCATGCTTGGGCAAGTAGGCTGGGCTGCTGCTGGCACTGCTGCTGCCCGGTGGTG 180
DB      121 CAGCCATGCTTGGGCAAGTAGGCTGGGCTGCTGCTGGCACTGCTGCTGCCCGGTGGTG 180

QY      181 GTGCTTCCACCGCAGGACCGTGTCCGACTCAACAGGAGGAGGAGGAGGAGGAGGAGG 240
DB      181 GTGCTTCCACCGCAGGACCGTGTCCGACTCAACAGGAGGAGGAGGAGGAGGAGGAGG 240

QY      241 AAATTGGGAAAGCCCTCTCCAGCGGGCCCTGAGGTCACTGTCCCTCAATTTCTGACT 300
DB      241 AAATTGGGAAAGCCCTCTCCAGCGGGCCCTGAGGTCACTGTCCCTCAATTTCTGACT 300
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QY      301 GGAGTGGAGAGGGCTTCCAGCCCAACAGATCGGATCTGATGTCCATGTGCCCCGCC 360
DB      301 GGAGTGGAGAGGGCTTCCAGCCCAACAGATCGGATCTGATGTCCATGTGCCCCGCC 360

QY      361 TCCACTGAAATTCATTGCTGCTGCGAGTGGCTGCTGCGAGCAGCAGCTAATTTACTT 420
DB      361 TCCACTGAAATTCATTGCTGCTGCGAGTGGCTGCTGCGAGCAGCAGCTAATTTACTT 420

QY      421 TCAAGTCTTTTGGGCCCCAGAGCCCTGAGCTGAGCTGCTGCTGAGAACCTGCTGCTG 480
DB      421 TCAAGTCTTTTGGGCCCCAGAGCCCTGAGCTGAGCTGCTGCTGAGAACCTGCTGCTG 480

QY      481 ACACCCGGGTGACCCAGAGCTCCATCAGAACCCCTGCTGCTGAGCATCTGCTGCTGCT 540
DB      481 ACACCCGGGTGACCCAGAGCTCCATCAGAACCCCTGCTGCTGAGCATCTGCTGCTGCT 540

QY      541 TATTCTCGGGCCACGCCCAACGAGTTTGTGAGTAAACAGTCTGCTGAGTAACTGCTGCT 600
DB      541 TATTCTCGGGCCACGCCCAACGAGTTTGTGAGTAAACAGTCTGCTGAGTAACTGCTGCT 600

QY      601 TCCTGGTGCAGAGCAGCATTAAGCTGCTTGTGAGTAAACAGTCTGCTGAGCATCTGCT 660
DB      601 TCCTGGTGCAGAGCAGCATTAAGCTGCTTGTGAGTAAACAGTCTGCTGAGCATCTGCT 660

QY      661 ACCTGGTGCAGGGTGTCAATGCTCCAGCTGGGACCTTAATTTGGGCTCAACCCGCTGCT 720
DB      661 ACCTGGTGCAGGGTGTCAATGCTCCAGCTGGGACCTTAATTTGGGCTCAACCCGCTGCT 720

QY      721 CTGAGTCCCAGATCCGCTATTCCATGCTCAGTGTGCCCACTGTCCAGTGAATCAATTT 780
DB      721 CTGAGTCCCAGATCCGCTATTCCATGCTCAGTGTGCCCACTGTCCAGTGAATCAATTT 780

QY      781 CCCTGGAAGTCAATGCTGCTCTCTGCTGGGAGAGCCCATCATCTGCTGCCAGGATG 840
DB      781 CCCTGGAAGTCAATGCTGCTCTCTGCTGGGAGAGCCCATCATCTGCTGCCAGGATG 840

QY      841 CCACCCCTTTTGTGTCGAAGGATGTGGGTACCGAGGGCTCCATGAGCCACCGTGGCC 900
DB      841 CCACCCCTTTTGTGTCGAAGGATGTGGGTACCGAGGGCTCCATGAGCCACCGTGGCC 900

QY      901 TCTCCAGAGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB      901 TCTCCAGAGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

QY      961 TGGACATCAAGGGCAGCTGAGGTGGATGAGCATCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB      961 TGGACATCAAGGGCAGCTGAGGTGGATGAGCATCTGCTGCTGCTGCTGCTGCTGCTG 1020

QY      1021 GGCTCATCCCGAGGCTGGCCCGCCAGTTTCCCGAGGCCCATGCTGCTGCTGCTGCTGCT 1080
DB      1021 GGCTCATCCCGAGGCTGGCCCGCCAGTTTCCCGAGGCCCATGCTGCTGCTGCTGCTGCT 1080

QY      1081 GGTGGGTGCAACCTGCTGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB      1081 GGTGGGTGCAACCTGCTGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

QY      1141 CCTTCGTGAGGTCTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB      1141 CCTTCGTGAGGTCTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

QY      1201 ATGTGTAGTGAATTTGAGATCTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB      1201 ATGTGTAGTGAATTTGAGATCTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

QY      1261 CTTCTGCTGGGAGTGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB      1261 CTTCTGCTGGGAGTGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

QY      1321 CAGATCAGGTGCGCACACTGATGGGCAAGCTTTTGGAGAGGAGCCCTGCTGCTGCTGCT 1380
DB      1321 CAGATCAGGTGCGCACACTGATGGGCAAGCTTTTGGAGAGGAGCCCTGCTGCTGCTGCT 1380
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QY 1381 ATGCTCTCTTGGCCATGGGAATTGGCTCCCTGGTGTGGTCAACCTCCACTATGTGGCC 1440
Db 1381 ATGCTCTCTTGGCCATGGGAATTGGCTCCCTGGTGTGGTCAACCTCCACTATGTGGCC 1440
QY 1441 CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACAGAGCT 1500
Db 1441 CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACAGAGCT 1500
QY 1501 GAGCAAGACCACTGGGAGGCTGAGAGTGGGCCAGCTCGCTGTCTCAGGCGAATTTCTCA 1560
Db 1501 GAGCAAGACCACTGGGAGGCTGAGAGTGGGCCAGCTCGCTGTCTCAGGCGAATTTCTCA 1560
QY 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACCATATCTAGTCAATCAACCAAGCTGGAC 1620
Db 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACCATATCTAGTCAATCAACCAAGCTGGAC 1620
QY 1621 TGCTTAGTGGGCTGTTTATCTTCTCTCCCTGAGTGGCTGGGTCTCCCTCACTTTGCC 1680
Db 1621 TGCTTAGTGGGCTGTTTATCTTCTCTCCCTGAGTGGCTGGGTCTCCCTCACTTTGCC 1680
QY 1681 CTTTCCCTTCTG 1740
Db 1681 CTTTCCCTTCTG 1740
QY 1741 CCCACCCAGGGGGAGCAGACTCTCTCTCAGGCTGTATAGACTTGCCTCTTTGCATTA 1800
Db 1741 CCCACCCAGGGGGAGCAGACTCTCTCTCAGGCTGTATAGACTTGCCTCTTTGCATTA 1800
QY 1801 AACCACTCTCTTGGAGTGC 1820
Db 1801 AACCACTCTCTTGGAGTGC 1820

RESULT 7

US-10-205-890-497
Sequence 497, Application US/10205890
Publication No. US20040048334A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P430R1C519
CURRENT APPLICATION NUMBER: US/10/205,890
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612

SEQ ID NO 497
LENGTH: 1820
TYPE: DNA
ORGANISM: Homo Sapien
US-10-205-890-497

Query Match 99.2%; Score 1816.8; DB 13; Length 1820;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCTTATAAGCTAGCTCTGCATCTGCCTGCTGGGAGGAGGCTTACCTGGGGCT 60
Db 1 GCCTTATAAGCTAGCTCTGCATCTGCCTGCTGGGAGGAGGCTTACCTGGGGCT 60
QY 61 GAGAGTTCACTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGGAGCGCCAGG 120
Db 61 GAGAGTTCACTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGGAGCGCCAGG 120
QY 121 CAGCATGGCTTGGCAAGTAGGCTGGCCCTGCTGTGGCACTGTCTGCTGGCTG 180
Db 121 CAGCATGGCTTGGCAAGTAGGCTGGCCCTGCTGTGGCACTGTCTGCTGGCTG 180
QY 181 GTGCTTCCAGCCAGGACCGTGTGGTCCGACTCAACAGGAGCAGATTGAGCTACGTG 240
Db 181 GTGCTTCCAGCCAGGACCGTGTGGTCCGACTCAACAGGAGCAGATTGAGCTACGTG 240
QY 241 AAATTGGGAAAGCCCTCTTCCAGGCGCCCTGCGAGGTCACCTGTCCCTCAATTTCTGG 300
Db 241 AAATTGGGAAAGCCCTCTTCCAGGCGCCCTGCGAGGTCACCTGTCCCTCAATTTCTGG 300
QY 301 GGAGTGAGAGGCGGCTTCCAGCCAGGATCCGAGTCTGAAATGTCATGTGCCCCGCC 360
Db 301 GGAGTGAGAGGCGGCTTCCAGCCAGGATCCGAGTCTGAAATGTCATGTGCCCCGCC 360
QY 361 TCCACCTGMAATTCATTTGCTGTTTCCGAGTGGCCCTGCTGGGAGCAGCTAATTTACT 420
Db 361 TCCACCTGMAATTCATTTGCTGTTTCCGAGTGGCCCTGCTGGGAGCAGCTAATTTACT 420
QY 421 TCAAGTCTTTTGGGCCCCAGAGCCCTTGGAGCTGAGCTGCTGCTGTGAACTGTGGCTG 480
Db 421 TCAAGTCTTTTGGGCCCCAGAGCCCTTGGAGCTGAGCTGCTGCTGTGAACTGTGGCTG 480
QY 481 ACACCCGGTGACCCAGAGCTCCATCAGGACCCCTGTGGTGTGAGCATCTCTGCTGCT 540
Db 481 ACACCCGGTGACCCAGAGCTCCATCAGGACCCCTGTGGTGTGAGCATCTCTGCTGCT 540
QY 541 TATTCTGGGCGCACGCCAAGAGTTTTCATGTCAGTAAACAGCCTCCACGCGCTGCTGG 600
Db 541 TATTCTGGGCGCACGCCAAGAGTTTTCATGTCAGTAAACAGCCTCCACGCGCTGCTGG 600
QY 601 TCTTGTGTCAGAGCACAATTAAGCTCTTTGAGTAAACAGCTGTGCTGAGCATCTCCA 660
Db 601 TCTTGTGTCAGAGCACAATTAAGCTCTTTGAGTAAACAGCTGTGCTGAGCATCTCCA 660
QY 661 ACCTGTGTCAGAGTGTCAATGTCCAGCTGAGCTTAAATGGGCTCAACCCGCTGGGTC 720
Db 661 ACCTGTGTCAGAGTGTCAATGTCCAGCTGAGCTTAAATGGGCTCAACCCGCTGGGTC 720
QY 721 CTGAGTCCAGAGTCCGCTATTTCCATGTGTGCGCCACTGTCCAGTGTACTACATTT 780
Db 721 CTGAGTCCAGAGTCCGCTATTTCCATGTGTGCGCCACTGTCCAGTGTACTACATTT 780
QY 781 CCTTGAAGTCAATGCTTCTTCTTCTGCTGGGCAACCCCACTCATCTGCCCCAGGATG 840
Db 781 CCTTGAAGTCAATGCTTCTTCTTCTGCTGGGCAACCCCACTCATCTGCCCCAGGATG 840
QY 841 CCACCCCTTTTGTGTCGCAAGGCAATGTGGGTACCGAGGCTCCATGGCCACCGTGGGCC 900
Db 841 CCACCCCTTTTGTGTCGCAAGGCAATGTGGGTACCGAGGCTCCATGGCCACCGTGGGCC 900

1 TITLE OF INVENTION: ACIDS ENCODING THE SAME
2 FILE REFERENCE: P3430R1C41
3 CURRENT APPLICATION NUMBER: US/1C/174,581
4 CURRENT FILING DATE: 2002-06-18
5 PRIOR APPLICATION NUMBER: 10/052586
6 PRIOR FILING DATE: 2002-01-15
7 PRIOR APPLICATION NUMBER: 60/059263
8 PRIOR FILING DATE: 1997-09-18
9 PRIOR APPLICATION NUMBER: 60/059266
10 PRIOR FILING DATE: 1997-09-18
11 PRIOR APPLICATION NUMBER: 60/062250
12 PRIOR FILING DATE: 1997-10-17
13 PRIOR APPLICATION NUMBER: 60/063120
14 PRIOR FILING DATE: 1997-10-24
15 PRIOR APPLICATION NUMBER: 60/063121
16 PRIOR FILING DATE: 1997-10-24
17 PRIOR APPLICATION NUMBER: 60/063486
18 PRIOR FILING DATE: 1997-10-21
19 PRIOR APPLICATION NUMBER: 60/063540
20 PRIOR FILING DATE: 1997-10-28
21 PRIOR APPLICATION NUMBER: 60/063541
22 PRIOR FILING DATE: 1997-10-28
23 PRIOR APPLICATION NUMBER: 60/063544
24 PRIOR FILING DATE: 1997-10-28
25 PRIOR APPLICATION NUMBER: 60/063564
26 PRIOR FILING DATE: 1997-10-28
27 PRIOR APPLICATION NUMBER: 60/063734
28 PRIOR FILING DATE: 1997-10-29
29 PRIOR APPLICATION NUMBER: 60/063870
30 PRIOR FILING DATE: 1997-10-31
31 PRIOR APPLICATION NUMBER: 60/064103
32 PRIOR FILING DATE: 1997-10-31
33 PRIOR APPLICATION NUMBER: 60/065311
34 PRIOR FILING DATE: 1997-11-13
35 PRIOR APPLICATION NUMBER: 60/066120
36 PRIOR FILING DATE: 1997-11-21
37 PRIOR APPLICATION NUMBER: 60/066466
38 PRIOR FILING DATE: 1997-11-24
39 PRIOR APPLICATION NUMBER: 60/066772
40 PRIOR FILING DATE: 1997-11-24
41 PRIOR APPLICATION NUMBER: 60/069335
42 PRIOR FILING DATE: 1997-12-11
43 PRIOR APPLICATION NUMBER: 60/069425
44 PRIOR FILING DATE: 1997-12-22
45 PRIOR APPLICATION NUMBER: 60/069870
46 PRIOR FILING DATE: 1997-12-17
47 PRIOR APPLICATION NUMBER: 60/068017
48 PRIOR FILING DATE: 1997-12-18
49 PRIOR APPLICATION NUMBER: 60/077450
50 PRIOR FILING DATE: 1998-03-10
51 PRIOR APPLICATION NUMBER: 60/077632
52 PRIOR FILING DATE: 1998-03-11
53 PRIOR APPLICATION NUMBER: 60/077649
54 PRIOR FILING DATE: 1998-03-11
55 PRIOR APPLICATION NUMBER: 60/078886
56 PRIOR FILING DATE: 1998-03-20
57 PRIOR APPLICATION NUMBER: 60/078939
58 PRIOR FILING DATE: 1998-03-20
59 PRIOR APPLICATION NUMBER: 60/079664
60 PRIOR FILING DATE: 1998-03-27
61 PRIOR APPLICATION NUMBER: 60/079786
62 PRIOR FILING DATE: 1998-03-27
63 PRIOR APPLICATION NUMBER: 60/080107
64 PRIOR FILING DATE: 1998-03-31
65 PRIOR APPLICATION NUMBER: 60/080194
66 PRIOR FILING DATE: 1998-03-31
67 PRIOR APPLICATION NUMBER: 60/080327
68 PRIOR FILING DATE: 1998-04-01
69 PRIOR APPLICATION NUMBER: 60/080333
70 PRIOR FILING DATE: 1998-04-01
71 PRIOR APPLICATION NUMBER: 60/081049
72 PRIOR FILING DATE: 1998-04-08
73 PRIOR APPLICATION NUMBER: 60/081070
74 PRIOR FILING DATE: 1998-04-08
75 PRIOR APPLICATION NUMBER: 60/081195
76 PRIOR FILING DATE: 1998-04-09
77 PRIOR APPLICATION NUMBER: 60/081838
78 PRIOR FILING DATE: 1998-04-15
79 PRIOR APPLICATION NUMBER: 60/082568
80 PRIOR FILING DATE: 1998-04-21
81 PRIOR APPLICATION NUMBER: 60/082569
82 PRIOR FILING DATE: 1998-04-21
83 PRIOR APPLICATION NUMBER: 60/082704
84 PRIOR FILING DATE: 1998-04-22
85 PRIOR APPLICATION NUMBER: 60/082797
86 PRIOR FILING DATE: 1998-04-22
87 PRIOR APPLICATION NUMBER: 60/083322
88 PRIOR FILING DATE: 1998-04-28
89 PRIOR APPLICATION NUMBER: 60/083495
90 PRIOR FILING DATE: 1998-04-29
91 PRIOR APPLICATION NUMBER: 60/083496
92 PRIOR FILING DATE: 1998-04-29
93 PRIOR APPLICATION NUMBER: 60/083499
94 PRIOR FILING DATE: 1998-04-29
95 PRIOR APPLICATION NUMBER: 60/083559
96 PRIOR FILING DATE: 1998-04-29
97 PRIOR APPLICATION NUMBER: 60/084366
98 PRIOR FILING DATE: 1998-05-05
99 PRIOR APPLICATION NUMBER: 60/084414
100 PRIOR FILING DATE: 1998-05-06
101 PRIOR APPLICATION NUMBER: 60/084639
102 PRIOR FILING DATE: 1998-05-07
103 PRIOR APPLICATION NUMBER: 60/084640
104 PRIOR FILING DATE: 1998-05-07
105 PRIOR APPLICATION NUMBER: 60/084643
106 PRIOR FILING DATE: 1998-05-07
107 PRIOR APPLICATION NUMBER: 60/085573
108 PRIOR FILING DATE: 1998-05-15
109 PRIOR APPLICATION NUMBER: 60/085579
110 PRIOR FILING DATE: 1998-05-15
111 PRIOR APPLICATION NUMBER: 60/085580
112 PRIOR FILING DATE: 1998-05-15
113 PRIOR APPLICATION NUMBER: 60/085582
114 PRIOR FILING DATE: 1998-05-15
115 PRIOR APPLICATION NUMBER: 60/085700
116 PRIOR FILING DATE: 1998-05-15
117 PRIOR APPLICATION NUMBER: 60/086023
118 PRIOR FILING DATE: 1998-05-18
119 PRIOR APPLICATION NUMBER: 60/086392
120 PRIOR FILING DATE: 1998-05-22
121 PRIOR APPLICATION NUMBER: 60/086486
122 PRIOR FILING DATE: 1998-05-22
123 PRIOR APPLICATION NUMBER: 60/087098
124 PRIOR FILING DATE: 1998-05-28
125 PRIOR APPLICATION NUMBER: 60/087208
126 PRIOR FILING DATE: 1998-05-28
127 PRIOR APPLICATION NUMBER: 60/087609
128 PRIOR FILING DATE: 1998-06-02
129 PRIOR APPLICATION NUMBER: 60/087759
130 PRIOR FILING DATE: 1998-06-02
131 PRIOR APPLICATION NUMBER: 60/087827
132 PRIOR FILING DATE: 1998-06-03
133 PRIOR APPLICATION NUMBER: 60/088025
134 PRIOR FILING DATE: 1998-06-04
135 PRIOR APPLICATION NUMBER: 60/088028
136 PRIOR FILING DATE: 1998-06-04
137 PRIOR APPLICATION NUMBER: 60/088029
138 PRIOR FILING DATE: 1998-06-04
139 PRIOR APPLICATION NUMBER: 60/088033
140 PRIOR FILING DATE: 1998-06-04
141 PRIOR APPLICATION NUMBER: 60/088167
142 PRIOR FILING DATE: 1998-06-05
143 PRIOR APPLICATION NUMBER: 60/088202
144 PRIOR FILING DATE: 1998-06-05
145 PRIOR APPLICATION NUMBER: 60/088212
146 PRIOR FILING DATE: 1998-06-05

Db 1321 CAGATCAGGTGGGCACTGATGGGACCCGTTTGTGAGAGCCCTGCTGGACCATCTCA 1380
QY 1381 ATGCTCTCTTGGCCATGGGAATTGCCCTCCCTGCTGGTGGTCAACTCTACTATCTGCCCC 1440
Db 1381 ACCTCTCTTGGCCATGGGAATTGCCCTCCCTGCTGGTGGTCAACTCTACTATCTGCCCC 1440
QY 1441 CTGAGATCTTGTCTATGAGGGCTACGCTGGTGTATCCAGTGGACTCTTCTACAGAGCT 1500
Db 1441 CTGAGATCTTGTCTATGAGGGCTACGCTGGTGTATCCAGTGGACTCTTCTACAGAGCT 1500
QY 1501 GAGCAAGACACTGGGAGCCCTGAGAGTGGGCCGCTGCTGCTCAGCGGAATTTCTCA 1560
Db 1501 GAGCAAGACACTGGGAGCCCTGAGAGTGGGCCGCTGCTGCTCAGCGGAATTTCTCA 1560
QY 1561 TTTCAAGCCACTGGGGAATCTAGGCAAAACCATCTAGTCTATCAACCAAGCTGGAC 1620
Db 1561 TTTCAAGCCACTGGGGAATCTAGGCAAAACCATCTAGTCTATCAACCAAGCTGGAC 1620
QY 1621 TGCTAGCTGGGCTGTTTATCTCCCTGAGTGGCTGGGCTGCTCCCTCACTTCTGCC 1680
Db 1621 TGCTAGCTGGGCTGTTTATCTCCCTGAGTGGCTGGGCTGCTCCCTCACTTCTGCC 1680
QY 1681 CTTCCT 1740
Db 1681 CTTCCT 1740
QY 1741 CCACCCCGAGGGGAGAGACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
Db 1741 CCACCCCGAGGGGAGAGACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
QY 1801 AACCACTCTCTGAGCTGC 1820
Db 1801 AACCACTCTCTGAGCTGC 1820

RESULT 12

US-10-176-749-497
; Sequence 497, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P343CRIC76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 497
; LENGTH: 1820
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-497

Query Match 99.2%; Score 1816.8; DB 13; Length 1820;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCTTATAAGTAGCTCTGATCTGCTGCTCGGCGAGAGAGGGCTACCTGGGGCT 60
Db 1 GCCTTATAAGTAGCTCTGATCTGCTGCTCGGCGAGAGAGGGCTACCTGGGGCT 60
QY 61 GAGAGTTCACTGCTCTCAGGACCACTGAGCCCAAGATCTCTGTGGCGAGGGCCAGGG 120

Db 61 GAGAGTTCACTGCTCTCAGGACCACTGAGCCCAAGATCTCTGTGGCGAGGGCCAGGG 120
QY 121 CAGGCATGGCTTGGGCAAGTAGGCTGGGCTGCTGTGGCACTGCTGCTGCTGCTGCTGCTG 180
Db 121 CAGGCATGGCTTGGGCAAGTAGGCTGGGCTGCTGTGGCACTGCTGCTGCTGCTGCTGCTG 180
QY 181 GTGCTCTCAGCCAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 GTGCTCTCAGCCAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AAATGGGAAAGCCCTCTCCAGCGGCCCTGCGAGGTCATCTGCTCCCTCACTTCTGAGCT 300
Db 241 AAATGGGAAAGCCCTCTCCAGCGGCCCTGCGAGGTCATCTGCTCCCTCACTTCTGAGCT 300
QY 301 GGAGTGGAGAGGCGCTCTCAGGCCCAAGAGATCCGATTCGATTCGATTCGATTCGATTC 360
Db 301 GGAGTGGAGAGGCGCTCTCAGGCCCAAGAGATCCGATTCGATTCGATTCGATTCGATTC 360
QY 361 TCCACCTGAAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 TCCACCTGAAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TCAAGTCTTTTGGGCGCCCAAGAGCCCTGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TCAAGTCTTTTGGGCGCCCAAGAGCCCTGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 ACACCCGCGTACCCAGAGCTCCATCAGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTT 540
Db 481 ACACCCGCGTACCCAGAGCTCCATCAGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTT 540
QY 541 TATTTCTGGGCCACGCCAAGAGTTTGTGAGGAGTAAACAGCACTCCACGCGCTGCTGG 600
Db 541 TATTTCTGGGCCACGCCAAGAGTTTGTGAGGAGTAAACAGCACTCCACGCGCTGCTGG 600
QY 601 TCTGCTGAGAGAGCAATTAAGCTGCTTGTAGTAAACAGCTGTGCTGCTGAGCATCTCCA 660
Db 601 TCTGCTGAGAGAGCAATTAAGCTGCTTGTAGTAAACAGCTGTGCTGCTGAGCATCTCCA 660
QY 661 ACTGCTGAGAGGCTGCAATGCTCCACTGGGCACTTAATGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ACTGCTGAGAGGCTGCAATGCTCCACTGGGCACTTAATGCTGCTGCTGCTGCTGCTGCT 720
QY 721 CTGAGTCCAGATCCGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 CTGAGTCCAGATCCGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CCTGGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 CCTGGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 CCACCCCTTTTGTGTTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 CCACCCCTTTTGTGTTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 TCTCCAGAGCTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 TCTCCAGAGCTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TGGACATCACAGGCGAGCTGAGTGGATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 TGGACATCACAGGCGAGCTGAGTGGATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 GGTCTCATCCCGAGGCTGGCCCGCCAGTTTCCCGAGCCATGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 GGTCTCATCCCGAGGCTGGCCCGCCAGTTTCCCGAGCCATGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 GGTCTGGTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1081 GGTCTGGTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 CCTTCTGAGAGGTTCTTGGCGCAGGCTGCACTCGGCTTTCAGTCCCTCTCTCTCTCTCT 1200

Db 1141 CCTCTGGAGGCTCTGGCCACAGCCTCCAACTGGCTTTCCAGTCCCTCTCTCCCTGG 1200
Qy 1201 ATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAAGGTGAAGCTTCAGGGGACCA 1260
Db 1201 ATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAAGGTGAAGCTTCAGGGGACCA 1260
Qy 1261 CGTCTGTGCTGGGGGATGTCCAGTCAAGGTGGCTCTCTCCAAAGGTGGGCTTCATTGATA 1320
Db 1261 CGTCTGTGCTGGGGGATGTCCAGTCAAGGTGGCTCTCTCCAAAGGTGGGCTTCATTGATA 1320
Qy 1321 CAGATCAGGTGGCGCACACTGATGGGACACCTGTTTGGAGAGCCCTCTCGACCATCTCA 1380
Db 1321 CAGATCAGGTGGCGCACACTGATGGGACACCTGTTTGGAGAGCCCTCTCGACCATCTCA 1380
Qy 1381 ATGCTCTCTGGCCATGGGAATGGCCCTCCCTGGTGTGGTCAACTCTCACTATGTGCCCC 1440
Db 1381 ATGCTCTCTGGCCATGGGAATGGCCCTCCCTGGTGTGGTCAACTCTCACTATGTGCCCC 1440
Qy 1441 CTGAGATCTTGTCTATGAGGGCTAGTGTGTATATCCAGTGACTTCTCAACAGACT 1500
Db 1441 CTGAGATCTTGTCTATGAGGGCTAGTGTGTATATCCAGTGACTTCTCAACAGACT 1500
Qy 1501 GAGGCAAGCACTGGGAGGCTGAGGTGGGCGAGCTCGCTCTCAGGCGAATTTCTCA 1560
Db 1501 GAGGCAAGCACTGGGAGGCTGAGGTGGGCGAGCTCGCTCTCAGGCGAATTTCTCA 1560
Qy 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACCATATCTAGTATCATCAACCAAGCTGGAC 1620
Db 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACCATATCTAGTATCATCAACCAAGCTGGAC 1620
Qy 1621 TGCTTAGCTGGGCTGTTTATCTCTCCCTGAGTGGCTGGGTCTCCCTCACTTCTGCC 1680
Db 1621 TGCTTAGCTGGGCTGTTTATCTCTCCCTGAGTGGCTGGGTCTCCCTCACTTCTGCC 1680
Qy 1681 CTTTCCCTTCCCT 1740
Db 1681 CTTTCCCTTCCCT 1740
Qy 1741 CCCACCCAGGGGGAGCAGACTGCTCTCCAGGCTGTATAGACTTCCCTCTCTCTCTCTCT 1800
Db 1741 CCCACCCAGGGGGAGCAGACTGCTCTCCAGGCTGTATAGACTTCCCTCTCTCTCTCTCT 1800
Qy 1801 AACCACTTCTCTTGAGCTGC 1820
Db 1801 AACCACTTCTCTTGAGCTGC 1820

RESULT 13

US-10-176-914-497
; Sequence 497, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 497
; LENGTH: 1820
; TYPE: DNA

; ORGANISM: Homo Sapien
US-10-176-914-497

Query Match
Best Local Similarity 99.2%; Score 1816.8; DB 13; Length 1820;
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCTTATAAGTAGCTCTGCTGCTGGGAGAGGGGTACCTGGGGCT 60
Db 1 GCCTTATAAGTAGCTCTGCTGCTGGGAGAGGGGTACCTGGGGCT 60
Qy 61 GAGAGTTTCACTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGCAGGCGCCAGG 120
Db 61 GAGAGTTTCACTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGCAGGCGCCAGG 120
Qy 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTCTGTGGCACTGTCTGCTGGCTGGTGG 180
Db 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTCTGTGGCACTGTCTGCTGGCTGGTGG 180
Qy 181 GTCCCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 240
Db 181 GTCCCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 240
Qy 241 AATTTGGGAAAGCCCTCTCCAGCGGCGCTTCCAGCGGCGCTGTCCAGGCTCACTTCTCT 300
Db 241 AATTTGGGAAAGCCCTCTCCAGCGGCGCTTCCAGCGGCGCTGTCCAGGCTCACTTCTCT 300
Qy 301 GGAGTGGAGAGGCGCTTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 360
Db 301 GGAGTGGAGAGGCGCTTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 360
Qy 361 TCCACCTGAATTCATGCTGTGGTTCGGAGTGGCGCTGTGGCAGCAGCTTAATTTTACTT 420
Db 361 TCCACCTGAATTCATGCTGTGGTTCGGAGTGGCGCTGTGGCAGCAGCTTAATTTTACTT 420
Qy 421 TCAAGTCTTTTCGGCGCCCGAGAGCCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 480
Db 421 TCAAGTCTTTTCGGCGCCCGAGAGCCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 480
Qy 481 ACACCGGCTGACCCAGAGCTCCATCAGGACCCCTGTGTGTGCTGAGCATCTCTGCTGCTCT 540
Db 481 ACACCGGCTGACCCAGAGCTCCATCAGGACCCCTGTGTGTGCTGAGCATCTCTGCTGCTCT 540
Qy 541 TATTTCTCGGGCCACCCAGAGCTTGTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 600
Db 541 TATTTCTCGGGCCACCCAGAGCTTGTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 600
Qy 601 TCTGGTGCAGAAAGCACATTAAGCTGTCTTCAAGTAAACAAGCTGTGCTGAGCATCTTCCA 660
Db 601 TCTGGTGCAGAAAGCACATTAAGCTGTCTTCAAGTAAACAAGCTGTGCTGAGCATCTTCCA 660
Qy 661 ACCTGGTGCAGGGTGTCAATGTCCAGCTGGGCACTTAAATTTGGCTCAACCCCGTGGGTC 720
Db 661 ACCTGGTGCAGGGTGTCAATGTCCAGCTGGGCACTTAAATTTGGCTCAACCCCGTGGGTC 720
Qy 721 CTGAGTCCAGATCCGCTTATTCATGTGCTGAGTGGCCCACTGTCAACAGTGAATCAATTT 780
Db 721 CTGAGTCCAGATCCGCTTATTCATGTGCTGAGTGGCCCACTGTCAACAGTGAATCAATTT 780
Qy 781 CCCTGGAAAGTCAATGCTGTCTTCTTCTGCTGGGCAAGCCCATCATCTGCTGCTGAGGATG 840
Db 781 CCCTGGAAAGTCAATGCTGTCTTCTTCTGCTGGGCAAGCCCATCATCTGCTGCTGAGGATG 840
Qy 841 CCACCCCTTTTGTGTTCCCAAGGCAATGGGTACCGAGGGCTCCATGGCCACCGTGGGCC 900
Db 841 CCACCCCTTTTGTGTTCCCAAGGCAATGGGTACCGAGGGCTCCATGGCCACCGTGGGCC 900
Qy 901 TCTCCAGAGCTGTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 TCTCCAGAGCTGTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Qy 961 TGGACATCAAGGCGAGCTGAGGTGGATGACAACTGCTGAAACACCTGCTGCTGCTGCTGCT 1020
Db 961 TGGACATCAAGGCGAGCTGAGGTGGATGACAACTGCTGAAACACCTGCTGCTGCTGCTGCT 1020

GenCore version: 5.1.6
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OK protein - protein search, using sw model

Run on: June 29, 2004, 10:54:39 ; Search time 59 seconds
(without alignments)
2193.335 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265

Sequence: 1 YAWASRLGLLALLPVVGA.....PEIFVYGVYVWISSGLFYQS 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2265	100.0	458	4 AAB74722	AAB74722 Human mem
2	2265	100.0	458	4 ABB08889	Abb08889 Human EPI
3	2265	100.0	458	4 AAU14479	AAU14479 Human COV
4	2265	100.0	458	4 AAU14243	AAU14243 Human COV
5	2265	100.0	458	5 AAU09947	AAU09947 Human (ne
6	2265	100.0	458	7 ADE85847	ADE85847 Human ant
7	2260	99.8	458	4 AAU29272	AAU29272 Human PRO
8	2260	99.8	458	4 ABB08888	Abb08888 Human EPI
9	2260	99.8	458	5 ABB84977	Abb84977 Human PRO
10	2260	99.8	458	5 ABB95583	Abb95583 Human ang
11	2260	99.8	458	6 ABU58648	ABU58648 Human PRO
12	2260	99.8	458	6 ABU88196	ABU88196 Novel hum
13	2260	99.8	458	6 ABU84511	ABU84511 Human sec
14	2260	99.8	458	6 ABR66385	ABR66385 Human sec
15	2260	99.8	458	6 ABR65775	ABR65775 Human sec
16	2260	99.8	458	6 ABU99715	ABU99715 Human sec
17	2260	99.8	458	6 ABU82954	ABU82954 Human PRO
18	2260	99.8	458	6 ABU90075	ABU90075 Novel hum
19	2260	99.8	458	6 ABR68324	ABR68324 Human sec
20	2260	99.8	458	6 ABU96377	ABU96377 Novel hum
21	2260	99.8	458	6 ABU92808	ABU92808 Human sec
22	2260	99.8	458	6 ABO08885	ABO08885 Human sec
23	2260	99.8	458	6 ABO02937	ABO02937 Human sec
24	2260	99.8	458	6 ABR75091	ABR75091 Human sec
25	2260	99.8	458	6 ABR94853	ABR94853 Human sec

RESULT 1

AAB74722

ID AAB74722 standard; protein; 458 AA.

XX AC AAB74722;

XX XX

DT 12-JUN-2001 (first entry)

XX DE Human membrane associated protein MEMAP-28.

XX KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;

KW anti-inflammatory; anticonvulsant; immunosuppressive; antidiarrheic;

KW antiarteriosclerotic; gene therapy; cell proliferative disorder;

KW autoimmune disorder; inflammatory disorder; neurological disorder;

KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;

KW epilepsy; diarrhoea.

XX OS Homo sapiens.

XX XX

PN WO200112662-A2.

XX XX

PD 22-FEB-2001.

XX XX

PF 14-AUG-2000; 2000WO-US022315.

XX XX

PR 17-AUG-1999; 99US-0149641P.

PR 09-NOV-1999; 99US-0164203P.

XX XX

PA (INCY-) INCYTE GENOMICS INC.

XX XX

PI Lai P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;

PI Baughn MR, Lu DAM, Patterson C;

XX XX

DR WPI; 2001-168860/17.

DR N-ESDB; AAF81768.

XX XX

PT Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders.

XX Claim 1: Page 139-140; 173pp; English.

PS AAF81741 to AAP81777 encode the human membrane associated proteins

XX (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,

CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and

CC antiarteriosclerotic activities, which can be used in gene therapy.

CC MEMAPs and agonists of MEMAPs can be used to treat a disease or condition

CC associated with decreased expression of functional MEMAP and antagonists

XX

of MEMAP are used to treat a disease or condition associated with overexpression of functional MEMAP. These disorders include cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders. The MEMAP polynucleotides and proteins are also used for the diagnosis of these disorders. Specific examples of these disorders include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea. MEMAP proteins can be used to screen for compounds which specifically bind MEMAP including antibodies, oligonucleotides, proteins and small molecules. MEMAP polynucleotides can be used to prepare transgenic animals which can be studied to provide information concerning human disease. Anti-MEMAP antibodies are useful in immunoassays for the detection of MEMAP protein and can be used as antagonists to treat or prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP can be delivered to target cells with genetic abnormalities with respect to the expression of MEMAP to treat or prevent a disorder associated with MEMAP

XX Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.7e-228;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGILLALLPVVGASTPGTVRLNKAALSVSEIGKAPLQALQVTPVPHFLDWS 60
DB 1 MAWASRLGILLALLPVVGASTPGTVRLNKAALSVSEIGKAPLQALQVTPVPHFLDWS 60

QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLLAANFTKVPRAPELELTLPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLLAANFTKVPRAPELELTLPVELLADT 120

QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVQKHKAVLSNKLCLISNLS 180
DB 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVQKHKAVLSNKLCLISNLS 180

QY 181 VGVNVHVLGTLGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
DB 181 VGVNVHVLGTLGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240

QY 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQSRSDNLLNTSALGRL 300
DB 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQSRSDNLLNTSALGRL 300

QY 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360

QY 361 VVNLRLQLSVSKVLQGTTSVLGDVQLTVASSNVGFIDTDQVRLMGTVFEKPLDLHLNA 420
DB 361 VVNLRLQLSVSKVLQGTTSVLGDVQLTVASSNVGFIDTDQVRLMGTVFEKPLDLHLNA 420

QY 421 LLAMGIALPGVNVHVAPEIFVYGVYVWISSGLFYQS 458
DB 421 LLAMGIALPGVNVHVAPEIFVYGVYVWISSGLFYQS 458

RESULT 2

ABB08889

XX ABB08889 standard; protein; 458 AA.

AC ABB08889;

DT 14-JUN-2002 (first entry)

XX Human BPIL 196-2 SEQ ID NO 4.

DE Human

XX Human; bactericidal/permeability increasing factor-like; BPIL;
KW antimicrobial; bactericidal; cytostatic; antileukaemia; antinflammatory;
KW immunomodulatory; infection; cancer; chemotactic; chemokinetic; cytokine;
KW cell proliferation; differentiation; immune response; gene therapy;
XX vaccine; protein coordinate data.

OS Homo sapiens.

XX WO200136478-A2.
PN 25-MAY-2001.
XX 20-NOV-2000; 2000WO-US031878.
XX 19-NOV-1999; 99US-00443370.
PR 18-JAN-2000; 2000US-00484597.
PR 22-FEB-2000; 2000US-0183922P.
PR 29-MAR-2000; 2000US-0193400P.
XX (HYSE-) HYSEQ INC.
XX Ballinger DG, Mulero JJ, Qian X, Mize NK, Haley DA, Boyle BJ;
XX MPI; 2001-381225/40.
DR N-PSDB; ABL55896.
XX Polypeptides with bactericidal/permeability increasing factor-like activity, the nucleic acids that encode them, useful for diagnosing and/or treating e.g. microbial infections and cancers.
XX Claim 29; Page 14-16; 807pp; English.
XX The invention relates to polypeptides (ABB08888-ABB08899) with bactericidal/permeability increasing factor-like (BPIL) activity, the nucleic acids that encode them (ABL55895-ABL55906) and methods and apparatus for detecting them and modulating their activity. The proteins have antimicrobial, bactericidal, cytostatic, antileukaemia, antinflammatory and immunomodulatory activity. The nucleic acids, polypeptides and methods may be used for detecting and treating pathologies associated with expression of BPIL polypeptides, e.g. for the treatment and diagnosis of microbial infections (especially by Gram negative bacterial, cancers (especially leukaemia), inflammation, disorders of chemotactic/chemokinetic activity and disorders of cytokine and cell proliferation/differentiation activity, to stimulate/suppress immune responses

XX Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.7e-228;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGILLALLPVVGASTPGTVRLNKAALSVSEIGKAPLQALQVTPVPHFLDWS 60
DB 1 MAWASRLGILLALLPVVGASTPGTVRLNKAALSVSEIGKAPLQALQVTPVPHFLDWS 60

QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLLAANFTKVPRAPELELTLPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLLAANFTKVPRAPELELTLPVELLADT 120

QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVQKHKAVLSNKLCLISNLS 180
DB 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVQKHKAVLSNKLCLISNLS 180

QY 181 VGVNVHVLGTLGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
DB 181 VGVNVHVLGTLGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240

QY 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQSRSDNLLNTSALGRL 300
DB 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQSRSDNLLNTSALGRL 300

QY 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360

QY 361 VVNLRLQLSVSKVLQGTTSVLGDVQLTVASSNVGFIDTDQVRLMGTVFEKPLDLHLNA 420
DB 361 VVNLRLQLSVSKVLQGTTSVLGDVQLTVASSNVGFIDTDQVRLMGTVFEKPLDLHLNA 420

PT nervous system disorders, and for regenerating bone and cartilage.
PS Example 4; Page 590-591; 894pp; English.
XX The invention relates to polynucleotides encoding novel human proteins or
XX their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides
CC polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/ elicit an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC diseases, nervous system disorders, and infection. The present sequence
XX represents a protein of the invention
SQ Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.7e-228;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
Db 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTKVPRAPELELTLPVELLADT 120
Db 61 GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTKVPRAPELELTLPVELLADT 120
QY 121 RVTOSSIRTPVVSISACSLFSGHANFPGNSNSTSHALLVLVQKHKAVLSNKLCLISNLL 180
Db 121 RVTOSSIRTPVVSISACSLFSGHANFPGNSNSTSHALLVLVQKHKAVLSNKLCLISNLL 180
QY 181 VQGVNVHLGTILGLNPVGPESQIRYSVMVSPVTVSDYISLEVNVLFLGKPIILPTDAT 240
Db 181 VQGVNVHLGTILGLNPVGPESQIRYSVMVSPVTVSDYISLEVNVLFLGKPIILPTDAT 240
QY 241 FVILPRHVGTGSMATVGLSQQLFDSALLLQKAGALNDITGQLRSDNLLNTSALGRL 300
Db 241 FVILPRHVGTGSMATVGLSQQLFDSALLLQKAGALNDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQFEEPMVVLKRLGATPVAMLTNATLRLQFFVEVLATASNSAFQSLFSLDV 360
Db 301 IPEVARQFEEPMVVLKRLGATPVAMLTNATLRLQFFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVQLQGTTSVLGQVLTAVSSNNGVFIQDQVRLMGTVFEKELLHLNA 420
Db 361 VVNLRLQLSVSKVQLQGTTSVLGQVLTAVSSNNGVFIQDQVRLMGTVFEKELLHLNA 420
QY 421 LLANGIALPGVNNLHYVAPEIFVYEGYVWISSGLFYQS 458
Db 421 LLANGIALPGVNNLHYVAPEIFVYEGYVWISSGLFYQS 458

RESULT 5
AAU09947
ID AAU09947 standard; protein; 458 AA.
XX

AC RAJF9947;
XX 18-JUN-2002 (first entry)
XX Human (new lipid binding protein 1) NLIBP1.
DE Human; new lipid binding protein 1; NLIBP1; cytostatic; antibacterial;
XX immunosuppressive; tranquilliser; vulnerary; haemostatic; cancer; tumour;
KW bacteraemia; endotoxaemia; meningococcal disease; haemorrhagic trauma;
KW partial hepatectomy; peritoneal infection; cystic fibrosis.
XX Homo sapiens.
OS WO2001077148-A2.
PN 18-OCT-2001.
XX 04-APR-2001; 2001WO-EP003794.
XX 05-APR-2000; 2000EP-00107354.
XX (MERE) MERCK PATENT GMBH.
PI Grell M, Duecker K, Hobeisel J, Frohme M;
XX WPI; 2002-010891/01.
DR N-PSDB; AAS15769.
XX New lipid binding protein 1 polypeptides and polynucleotides useful for
PT diagnosis and treatment of cancer, bacteraemia, endotoxaemia, peritoneal
PT infections, cystic fibrosis and identifying modulators of therapeutic
PT use.
PS Claim 2; Page 36; 36pp; English.
XX The present invention relates to a new isolated lipid binding protein 1
CC (NLIBP1) polypeptide chosen from a 458 residue amino acid sequence, fully
CC defined in the specification, a polypeptide comprising or having 95 %
CC identity to the 458 residue amino acid, fragments or variants of NLIBP1
CC and a polypeptide encoded by a 1812 base pair sequence, also fully
CC defined in the specification. NLIBP1 polypeptide is useful in screening
CC assays to identify compounds that stimulate or inhibit the function or
CC level of the polypeptide. NLIBP1 polypeptides, polynucleotides and their
CC agonists and antagonists are useful for treating cancer, bacteraemia,
CC endotoxaemia, meningococcal disease, haemorrhagic trauma, partial
CC hepatectomy, severe peritoneal infections and cystic fibrosis. The NLIBP1
CC polypeptides and polynucleotides are also useful as vaccines. NLIBP1
CC polypeptides are useful for identifying membrane bound or soluble
CC receptors. The molecules of the invention are useful for the recombinant
CC production of NLIBP1 polypeptides, in diagnostic assays by detecting
CC mutations in the associated gene, for chromosome localisation studies,
CC tissue expression studies and for producing transgenic animals useful in
CC drug discovery and target validation. The present sequence represents the
CC new lipid binding protein 1 (NLIBP1) that was used in the methods of the
CC invention
SQ Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 5; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.7e-228;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
Db 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTKVPRAPELELTLPVELLADT 120
Db 61 GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTKVPRAPELELTLPVELLADT 120
QY 121 RVTOSSIRTPVVSISACSLFSGHANFPGNSNSTSHALLVLVQKHKAVLSNKLCLISNLL 180
Db 121 RVTOSSIRTPVVSISACSLFSGHANFPGNSNSTSHALLVLVQKHKAVLSNKLCLISNLL 180

QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
 Db 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
 QY 241 PFVLPFRHVGTSGMATVGLSQQLFSDALLQKAGALNLDITGQRLSDNLLNTSALGRL 300
 Db 241 PFVLPFRHVGTSGMATVGLSQQLFSDALLQKAGALNLDITGQRLSDNLLNTSALGRL 300
 QY 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFOSLFLSDV 360
 Db 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFOSLFLSDV 360
 QY 361 VVNLRLQLSVSKVKLQGTTSVLGDLQVLTASSNVGFIQDTQVRLMGTVFEKPLDLHLNA 420
 Db 361 VVNLRLQLSVSKVKLQGTTSVLGDLQVLTASSNVGFIQDTQVRLMGTVFEKPLDLHLNA 420
 QY 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVYVSSGLFYQS 458
 Db 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVYVSSGLFYQS 458

RESULT 6
 ADE85847
 ID ADE85847 standard; protein; 458 AA.

XX ADE85847;
 AC
 XX
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human antibacterial polypeptide LPLUNC2.
 XX
 XX Human; antibacterial; LPLUNC2; PLUNC.
 XX
 XX Homo sapiens.
 OS
 XX WO2003087143-A2.
 PN
 XX
 XX 23-OCT-2003.
 PD
 XX
 XX 11-APR-2003; 2003WO-GB001583.
 EF
 XX
 XX 12-APR-2002; 2002GB-00008925.
 PR
 XX
 XX (UYSH-) UNIV SHEFFIELD.
 PA
 XX
 XX Bingle C, Craven J;
 PI
 XX
 XX WPI; 2003-833705/77.
 DR
 XX

New polypeptides encoded by nucleic acids that map to human chromosome 20q11, useful for treating bacterial infections, e.g. septicemia, tuberculosis, bacteria-associated food poisoning, blood infections, peritonitis.

Disclosure; Fig 2: 40pp; English.

The present sequence is the protein sequence of human antibacterial polypeptide LPLUNC2. The invention describes a family of 9 human proteins ADE85846-ADE85857 designated as PLUNCs (palate lung and nasal epithelium core) that are encoded by adjacent genes in an approximately 300 kb region on chromosome 20q11. Members of the PLUNC family fall into 2 groups based on their size. Short PLUNCs (SPLUNCs) comprise SPLUNC1, SPLUNC2, SPLUNC3 and SPLUNC7, while long PLUNCs (LPLUNCs) comprise LPLUNC1, LPLUNC2, LPLUNC3, LPLUNC4 and LPLUNC6. The polypeptides can be used to treat bacterial infections, in particular respiratory infections. The infection is caused by *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Mycobacterium tuberculosis*, *Streptococcus group B*, *Streptococcus pneumoniae*, *Helicobacter pylori*, *Neisseria gonorrhoea*, *Streptococcus group A*, *Borrelia burgdorferi*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Neisseria meningitidis* type B, *Shigella flexneri*, *Escherichia coli*, *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Pseudomonas aeruginosa*, *Legionella spp.*, *Moraxella*

CC catarrhalis, *Klebsiella pneumoniae*, *Fusobacterium nucleatum* or
 CC *Porphyromonas gingivalis*, and is septicemia, tuberculosis, bacteria-
 CC associated food poisoning, blood infection, peritonitis, endocarditis,
 CC sepsis, meningitis, pneumonia, stomach ulcer, gonorrhoea, step throat,
 CC streptococcal-associated toxic shock, necrotizing fascitis, impetigo,
 CC histoplasmosis, Lyme disease, gastro-enteritis, dysentery, shigellosis,
 CC or periodontal disease (all claimed).
 XX

SQ Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 7; Length 458;
 Best Local Similarity 100.0%; Pred. No. 7.7e-228;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLPVVGCSTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
 Db 1 MAWASRLGLLALLPVVGCSTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
 QY 61 GEALQPTIRILNVHVRHLKFIAGFGRVLLAANFTFKVFRAPPELTLPEVLLADT 120
 Db 61 GEALQPTIRILNVHVRHLKFIAGFGRVLLAANFTFKVFRAPPELTLPEVLLADT 120
 QY 121 RVTQSSIRTPVVISACSLFSGHANFDCGNSGTSHALLVVKHKAIVLSNKLCLISNL 180
 Db 121 RVTQSSIRTPVVISACSLFSGHANFDCGNSGTSHALLVVKHKAIVLSNKLCLISNL 180
 QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
 Db 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
 QY 241 PFVLPFRHVGTSGMATVGLSQQLFSDALLQKAGALNLDITGQRLSDNLLNTSALGRL 300
 Db 241 PFVLPFRHVGTSGMATVGLSQQLFSDALLQKAGALNLDITGQRLSDNLLNTSALGRL 300
 QY 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFOSLFLSDV 360
 Db 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFOSLFLSDV 360
 QY 361 VVNLRLQLSVSKVKLQGTTSVLGDLQVLTASSNVGFIQDTQVRLMGTVFEKPLDLHLNA 420
 Db 361 VVNLRLQLSVSKVKLQGTTSVLGDLQVLTASSNVGFIQDTQVRLMGTVFEKPLDLHLNA 420
 QY 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVYVSSGLFYQS 458
 Db 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVYVSSGLFYQS 458

RESULT 7
 AAU29272
 ID AAU29272 standard; protein; 458 AA.
 XX
 AC AAU29272;
 XX
 XX 18-DEC-2001 (first entry)
 DT
 XX
 DE Human PRO polypeptide sequence #249.
 XX

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

Homo sapiens.
 OS
 XX WO200168848-A2.
 PN
 XX
 XX 20-SEP-2001.
 PD
 XX
 XX 28-FEB-2001; 2001WO-US006520.
 PF
 XX
 XX 01-MAR-2000; 2000WO-US005601.
 PR
 XX 02-MAR-2000; 2000WO-US005841.
 PR
 XX 03-MAR-2000; 2000US-0187202P.
 PR

PR 06-MAR-2000; 2000US-0186568P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0180828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 FA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-602746/68.
 DR N-PSDB; AAS46173.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 498; 774pp; English.
 PS Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 458 AA;
 SQ Query Match
 Best Local Similarity 99.8%; Score 2260; DB 4; Length 458;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAAALSVVSEIGKAPLQALQVTVPHFLDWS 60
 DB 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAAALSVVSEIGKAPLQALQVTVPHFLDWS 60
 QY 61 GEALQPTRIRILNVHVPRIHLKFIAGFGVRLIAAANFTFKVPRAPPELELTLPVELLADT 120
 DB 61 GEALQPTRIRILNVHVPRIHLKFIAGFGVRLIAAANFTFKVPRAPPELELTLPVELLADT 120
 QY 121 RVTQSSIRTPVVSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
 DB 121 RVTQSSIRTPVVSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
 QY 181 VQGVNVHLGLTILGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLELIGKPIILPTDAT 240
 DB 181 VQGVNVHLGLTILGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLELIGKPIILPTDAT 240
 QY 241 PFVLPFRHVGTGSGMATVGLSQOLPDSALLLQKAGALNDITGQSRSDNLTNTSALGSL 300
 DB 241 PFVLPFRHVGTGSGMATVGLSQOLPDSALLLQKAGALNDITGQSRSDNLTNTSALGSL 300
 QY 301 IPEVARQPEEPMPVVLKVLGATPVAMLHTNATLRLQPFVEVLATASNAFQSLFSLDV 360
 DB 301 IPEVARQPEEPMPVVLKVLGATPVAMLHTNATLRLQPFVEVLATASNAFQSLFSLDV 360
 QY 361 VVNLRLQLSVSKVKLQGTTSVLGVDVQLTVASSNVGFIQDQVRLTMGTVEFKPLLDHLNA 420
 DB 361 VVNLRLQLSVSKVKLQGTTSVLGVDVQLTVASSNVGFIQDQVRLTMGTVEFKPLLDHLNA 420
 QY 421 LLAMGIALPGVNLHYVAPEIFVVEGYVVISGLFYQS 458
 DB 421 LLAMGIALPGVNLHYVAPEIFVVEGYVVISGLFYQS 458

RESULT 8

ABB08888
 ID ABB08888 standard; protein; 458 AA.

XX ABB08888;
 XX 14-JUN-2002 (first entry)
 XX Human BPIL 196-1 SEQ ID NO 2.
 XX Human; bactericidal/permeability increasing factor-like; BPII;
 XX antimicrobial; bactericidal; cytostatic; antileukaemia; antiinflammatory;
 XX immunomodulatory; infection; cancer; chemotactic; chemokinetic; cytokine;
 XX cell proliferation; differentiation; immune response; gene therapy;
 XX vaccine; protein coordinate data.

XX Homo sapiens.

XX WO200136478-A2.

XX 25-MAY-2001.

XX 20-NOV-2000; 2000WO-US031878.

XX 19-NOV-1999; 99US-00443370.

XX 18-JAN-2000; 2000US-00484597.

XX 22-FEB-2000; 2000US-0183922P.

XX 29-MAR-2000; 2000US-0193400P.

XX (HYSE-) HYSEQ INC.

XX Ballinger DG, Mulero JJ, Qian X, Mize NK, Haley DA, Boyle BJ;

XX WPI; 2001-381225/40.

XX N-PSDB; ABL55895.

XX Polypeptides with bactericidal/permeability increasing factor-like
 PT activity, the nucleic acids that encode them, useful for diagnosing
 PT and/or treating e.g. microbial infections and cancers.

XX Claim 29; Page 10-12; 807pp; English.

XX The invention relates to polypeptides (ABB08488-ABB08499) with

XX bactericidal/permeability increasing factor-like (BPI/L) activity, the

XX nucleic acids that encode them (ABL55895-ABL55906) and methods and

XX apparatus for detecting them and modulating their activity. The proteins

XX have antimicrobial, bactericidal, cytostatic, antileukaemia,

XX antiinflammatory and immunomodulatory activity. The nucleic acids,

XX polypeptides and methods may be used for detecting and treating

XX pathologies associated with expression of BPI/L polypeptides, e.g. for the

XX treatment and diagnosis of microbial infections (especially by Gram

XX negative bacteria), cancers (especially leukaemia), inflammation,

XX disorders of chemotactic/chemokinetic activity and disorders of cytokine

XX and cell proliferation/differentiation activity, to stimulate/suppress

XX immune responses

XX Sequence 458 AA;

Query Match 99.8%; Score 2260; DB 4; Length 458;

Best Local Similarity 99.8%; Pred. No. 2.6e-227;

Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGILLALLPVVGASTPGTGVRLNKAALSVSEIGKAPLQALQVTPHFLDWS 60

DB 1 MAWASRLGILLALLPVVGASTPGTGVRLNKAALSVSEIGKAPLQALQVTPHFLDWS 60

QY 61 GEALQPTIRILNVHVRHLKFIAGFGVRLIAAANFTPKVFAPEPLELTLPVELLADT 120

DB 61 GEALQPTIRILNVHVRHLKFIAGFGVRLIAAANFTPKVFAPEPLELTLPVELLADT 120

QY 121 RVTQSSIRTPVVISACSLFSGHANEFDGNSNSTSHALLVVKHKAVLSNKLCLSTSNL 180

DB 121 RVTQSSIRTPVVISACSLFSGHANEFDGNSNSTSHALLVVKHKAVLSNKLCLSTSNL 180

QY 131 VQGVNVHGLTILGLNPVGPESQIRVSMVSPVPTSDYISLEVNVLFLGKPIILPTDAT 240

DB 131 VQGVNVHGLTILGLNPVGPESQIRVSMVSPVPTSDYISLEVNVLFLGKPIILPTDAT 240

QY 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300

DB 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300

QY 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATANSAPQSIFSLDV 360

DB 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATANSAPQSIFSLDV 360

QY 361 VVNLRLQLSVSKVLQGTTSVLGDVQVLTAVSSNVGFIQDQVRLTNGTVEKPLLDHLNA 420

DB 361 VVNLRLQLSVSKVLQGTTSVLGDVQVLTAVSSNVGFIQDQVRLTNGTVEKPLLDHLNA 420

QY 421 LLAMGIALPGVVNLHYVAPEIFVYEGYVVVSSGLFYQS 458

DB 421 LLAMGIALPGVVNLHYVAPEIFVYEGYVVVSSGLFYQS 458

RESULT 9

ABB84977

ID ABB84977 standard; protein; 458 AA.

XX ABB84977;

XX ABB84977;

XX 16-MAY-2002 (first entry)

XX Human PRO5776 protein sequence SEQ ID NO:322.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

XX vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX age-related macular degeneration; arterial restenosis; angina;

XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

KW wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

OS WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US023710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2000US-00767609.

XX 28-FEB-2001; 2000US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 25-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 30-MAY-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017800.

XX {GETH } GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;

XX WPI: 2002-090516/12.

XX N-PSDB; ABL88232.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 322; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,

XX antiangiogenic, hypotensive, vulnery and antiarteriosclerotic

XX activities, and can be used in gene therapy. The PRO polynucleotides,

XX proteins, agonists and antagonists are useful for treating or diagnosing

XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The PRO polynucleotides have applications in molecular biology,

XX including use as hybridisation probes, and in chromosome and gene

```

CC mapping, ABL88259 to ABL88267 represent primers and probes used in the
CC exonification of the present invention
XX
SQ Sequence 458 AA;

Query Match          99.8%; Score 2260; DB 5; Length 458;
Best Local Similarity 99.8%; Pred. No. 2.6e-227;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGILLALLPVVGASTGTGTVRLNKAALSYSEIGKAPLQALQVTVPHPLDWS 60
DB 1 MAWASRLGILLALLPVVGASTGTGTVRLNKAALSYSEIGKAPLQALQVTVPHPLDWS 60

QY 61 GEAQLOPTRIRILNVHVRHLHAFIAGFGVRLAAANFTKVFRAPELELTLPVELLADT 120
DB 61 GEAQLOPTRIRILNVHVRHLHAFIAGFGVRLAAANFTKVFRAPELELTLPVELLADT 120

QY 121 RVTQSSIRTPVVISACSLFSGHANFQGSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
DB 121 RVTQSSIRTPVVISACSLFSGHANFQGSNSTSHALLVLVQKHIAVLSNKLCLISINL 180

QY 181 VQGVNVHLGTLGLNPVGPESQIRYSWVSPVPTSDYISLENAVLFLLGKPIILPTDAT 240
DB 181 VQGVNVHLGTLGLNPVGPESQIRYSWVSPVPTSDYISLENAVLFLLGKPIILPTDAT 240

QY 241 PFVLPFRHVCTEGSMATVGLSQFLDSALLLQKAGALNLDITGQLRSDNLTNTSALGRL 300
DB 241 PFVLPFRHVCTEGSMATVGLSQFLDSALLLQKAGALNLDITGQLRSDNLTNTSALGRL 300

QY 301 IPEVARQFPEPMPVVKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQFPEPMPVVKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360

QY 361 VVNLRLQLSVSKVKGQTTSVLGDVOLTVAASNNGFIDTDQVRLMGTVPEKPLLDHLNA 420
DB 361 VVNLRLQLSVSKVKGQTTSVLGDVOLTVAASNNGFIDTDQVRLMGTVPEKPLLDHLNA 420

QY 421 LLAAGIALPGVNLNHYVAPEIFVYEGYVVISGLFYQS 458
DB 421 LLAAGIALPGVNLNHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 10
ID ABB95583
AC ABB95583;
XX ABB95583;
XX ABB95583;
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO5776 SEQ ID NO: 322.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.

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PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.

```

{GETH } GENENTECH INC.

{BAKE } BAKER K P.

{FERR } FERRARA N.

{GERB } GERBER H.

{GERR } GERRITSEN M E.

{GODD } GODDARD A.

{GODO } GODOWSKI P J.

{GURN } GURNEY A L.

{HILL } HILLAN K J.

{MARS } MARSTERS S A.

{PANU } PAN J.

{PAON } PAONI N F.

{STEP } STEPHAN J F.

{WATA } WATANABE C K.

{WILL } WILLIAMS P M.

{WOOD } WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-171999/22.

N-PSDB; ABL95721.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,

useful in diagnosis and treatment of cardiovascular (e.g. myocardial

infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 322; 567pp; English.

XX

XX The present invention provides the protein and coding sequences of human

PRO proteins. These are useful for treating or diagnosing a

cardiovascular, endothelial or angiogenic disorder, including cardiac

hypertrophy, trauma, cancer, age-related macular degeneration,

atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention

XX

SQ Sequence 458 AA;

Query Match 99.8%; Score 2260; DB 5; Length 458;

Best Local Similarity 99.8%; Pred. No. 2.6e-227;

Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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QY 1 MAWASRLGULLALLLPVVGASTPGTVRLNKAALSVSEIGKAPLQALQVTVPHFELWS 60
DB 1 MAWASRLGULLALLLPVVGASTPGTVRLNKAALSVSEIGKAPLQALQVTVPHFELWS 60
QY 61 GEALOPTRIILNVHVRHLKFIAGFGVLLAAANFTKVFRAPEPLELTLPVELLAT 120
DB 61 GEALOPTRIILNVHVRHLKFIAGFGVLLAAANFTKVFRAPEPLELTLPVELLAT 120
QY 221 RYQSSIRTPVVSISACSLFSGHANFEDGSNSTSHALLVLVQKHAKAVLSNKLCLISINL 180
DB 221 RYQSSIRTPVVSISACSLFSGHANFEDGSNSTSHALLVLVQKHAKAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLFLLGKPIILPTDAT 240
DB 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLFLLGKPIILPTDAT 240
QY 241 PVLPRHVCTEGSMATVGLSQOLFSAALLQKAGALNLDITGQLSDNLLNTSALGRL 300
DB 241 PVLPRHVCTEGSMATVGLSQOLFSAALLQKAGALNLDITGQLSDNLLNTSALGRL 300
QY 301 IFEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLOPFVEVLATASNSAFOSLFSLDV 360
DB 301 IFEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLOPFVEVLATASNSAFOSLFSLDV 360
QY 361 VVNLRLQLSVSKVLOGTTSVLGDVOLTVAASNVGFIIDTVRTLMGTVPFKPPLLDHNA 420
DB 361 VVNLRLQLSVSKVLOGTTSVLGDVOLTVAASNVGFIIDTVRTLMGTVPFKPPLLDHNA 420
QY 421 LLAMGIALPGVNVHLVAPEIFVYEGYVVISGLFYQS 458
DB 421 LLAMGIALPGVNVHLVAPEIFVYEGYVVISGLFYQS 458

RESULT 11
ABU58648
ID ABU58648 standard; protein; 458 AA.
XX
AC ABU58648;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #249.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 29-OCT-1997; 97US-0063564P.
PR 31-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063878P.
PR 13-NOV-1997; 97US-0064103P.
PR 21-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066120P.
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Db 301 IPEVARQFPEPMPVVLKVELGATPVAMLTNNATLRLQPFVEVLATASNASFOSLSLDV 360
QY 361 VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGPDIDQVRTLMTGTVFEKPLLDHNA 420
Db 361 VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGPDIDQVRTLMTGTVFEKPLLDHNA 420
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISSGLFYQS 458
Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISSGLFYQS 458

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ABU88196
ID ABU88196 standard; protein; 458 AA.
XX AC ABU88196;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO5776.
XX KW Human; secreted and transmembrane protein; PRO; gene therapy;
XX KW tumour necrosis factor-alpha release; TNF-alpha release;
XX KW chondrocyte proliferation; chondrocyte differentiation; tumour;
XX KW adrenal tumour; lung tumour; colon tumour; breast tumour;
XX KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.

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RESULT 13
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XX AC ABU84511;
XX DT 02-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #249.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX KW tissue typing.
XX OS Homo sapiens.
XX PN US2003032112-A1.
XX PD 13-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176756.
XX PR 18-SEP-1997; 97US-0059263P.
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DB 61 GEALQPTIRILNVHVRHLKFTIAGFCVRLAAANFTKVFRAPEPELETLPVLELLADT 120
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Db 241 FVLPRHVGTEGSAWGLSQQFDSALLLQKAGALNLDITGQRSDNLLNTSALGRL 300
Qy 301 IPEVARQFPEPMPVVLKVRIGATVAMLTNNATRLQPFVEVLATASNSAFQSLFSLDV 360
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Qy 361 VVNLRLQLSVKVKGQTTSVLGDVQVLTVAASSNVGFDITDQVRLTMTGTFVEKPLLDHNA 420
Db 361 VVNLRLQLSVKVKGQTTSVLGDVQVLTVAASSNVGFDITDQVRLTMTGTFVEKPLLDHNA 420
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RESULT 14
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AC ABR66385;
DX XX
DT XX
DE XX
DE Human secreted polypeptide PRO5776, SEQ ID NO:498.
XX Human;
XX Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnery; gene therapy.
OS Homo sapiens.
XX
XX
PN US2003027278-A1.
XX
XX
PD 06-FEB-2003.
XX
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PF 21-JUN-2002; 2002US-00176987.
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Best Local Similarity 99.8%; Pred. No. 2,66-227;
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DB 61 GEALQPTRIRILNVHVPRLHLKFTAGFGVRLAAANFTKVFRAPEPELELTPVELLADT 120
QY 121 RVTQSSIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVQKHKAVLSNKLCLISINL 180
DB 121 RVTQSSIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVQKHKAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
QY 241 PFVLPRLHWTEGSMATVGLSQQLFDSALLQKAGALNLTITQOLRSDDDLNTSALGRL 300
DB 241 PFVLPRLHWTEGSMATVGLSQQLFDSALLQKAGALNLTITQOLRSDDDLNTSALGRL 300
QY 301 IPEVARQFPEPMPVVLKVRIGATPVAMLTNNATLRLQPFVEVLATASNAFQSLFLSDV 360
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DB 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISSGLFYQS 458

RESULT 15
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AC ABR65775;
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DE Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnery; gene therapy.
OS Homo sapiens.
XX US2003036159-A1.
XX 20-FEB-2003.
XX 02-JUL-2002; 2002US-00188773.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.

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PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
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PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
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PR	16-SEP-1998;	98US-0101751P.	
PR	16-SEP-1998;	98MO-US013330.	
PR	17-SEP-1998;	98US-0100683P.	
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PR	17-SEP-1998;	98US-0100330P.	
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PR	01-OCT-1998;	98US-0102687P.	
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Best Local Similarity 99.8%; Pred. No. 2,6e-227;			
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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Db	1	MAWASRLGLLLALLLPWGASTGTVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS	60
QY	61	GEALQPTRILNVHVRHLKFIAGVGVLLAAANFTKVPFAPPELTLTPVELLADT	120
Db	61	GEALQPTRILNVHVRHLKFIAGVGVLLAAANFTKVPFAPPELTLTPVELLADT	120
QY	121	RVTOSSIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVQKHKAVLSNKLCLGISNL	180
Db	121	RVTOSSIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVQKHKAVLSNKLCLGISNL	180
QY	181	VQGVNVHLGTLIGLNPVGPESQIRYSNVSVPTVTSYISLEVNVLFLGKPIILPTDAT	240
Db	181	VQGVNVHLGTLIGLNPVGPESQIRYSNVSVPTVTSYISLEVNVLFLGKPIILPTDAT	240
QY	241	PFVLPRHVGTGSMATVGLSQQLFDSALLLOKAGALNLDITGCLRSDDNLLNTSALGRL	300
Db	241	PFVLPRHVGTGSMATVGLSQQLFDSALLLOKAGALNLDITGCLRSDDNLLNTSALGRL	300
QY	301	IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATLRLQPEVEVLATASNSAFQSLFSLDV	360
Db	301	IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATLRLQPEVEVLATASNSAFQSLFSLDV	360
QY	361	VYKRLQLSVSKVKLGTTSVLGDVOLTVAASNVGFIIDQVRLMGTVPFEPKLLDHLNA	420
Db	361	VYKRLQLSVSKVKLGTTSVLGDVOLTVAASNVGFIIDQVRLMGTVPFEPKLLDHLNA	420
QY	421	LLAMGIALPGVNVNLHVVAPEIFVYEGVWVWISSGLFYQS	458
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Search completed: June 29, 2004, 10:58:54
Job time : 62 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2004, 21:30:21 ; Search time 7112 Seconds

(without alignments)

7688.084 Million cell updates/sec

Title: US-10-069-034-65

Perfect score: 1831

Sequence: 1 gcctataaagtagcctctg.....ttgsgctgcacaaaaaaa 1831

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hcc.*

9: gb_estl.*

10: gb_est2.*

11: gb_hcc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_fur.*

18: em_gss_inv.*

19: em_gss_p.h.*

20: em_gss_vit.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1377	75.2	1377	29	AY417102 Homo sapi
2	1314	71.8	1377	29	AY417103 Pan trogl
3	875.2	47.8	1703	11	AK009619 Mus muscu
4	875.2	47.8	1705	11	AK028158 Mus muscu

5	874.6	47.8	1696	11	AK009346
6	870.4	47.5	1699	11	AK075874
7	868.8	47.4	1701	11	AK028156
8	856.2	46.8	1679	11	AK010130
9	854.4	46.7	1693	11	AK010215
10	853.4	46.6	1688	11	AK009776
11	853	46.6	1727	11	AK010157
12	849.2	46.4	1698	11	AK010154
13	848	46.3	1700	11	AK009504
14	815.6	44.5	1389	29	AY417104
15	812.6	44.4	1699	11	AK009871
16	800.6	43.7	1688	11	AK009794
17	769.8	42.0	819	12	BI489783
18	677	37.0	1307	11	AK009754
19	560.4	30.6	578	13	EX487536
20	539	29.4	539	13	EX280449
21	477.8	26.1	1003	13	BY789668
22	466.2	25.5	883	13	BY709288
23	464	25.3	1013	13	BY709115
24	463.2	25.3	480	9	AJ403124
25	454.4	24.8	998	13	BY709211
26	435.6	23.8	453	9	AJ403122
27	423.2	23.4	982	13	BY709415
28	403.4	22.3	427	14	CD697627
29	396.8	21.7	737	10	BB610562
30	388.6	21.2	729	10	BB610508
31	371.6	20.3	712	10	BB610518
32	371.6	20.3	754	10	BB610661
33	296.2	18.2	650	12	BI490756
34	292.8	18.0	757	9	AV090749
35	291.6	15.9	747	9	AV089480
36	284.8	15.6	556	10	BB610620
37	277.4	15.2	543	10	BB610635
38	273.8	15.0	750	9	AV092418
39	239.8	13.1	589	12	BI279481
40	221.8	12.1	225	10	AW155639
41	179.8	9.8	184	9	AI834221
42	130.8	7.1	293	10	BB565312
43	122.4	6.7	146	10	AW444867
44	120.4	6.6	128	10	BF512164
45	119.6	6.5	279	10	BB565532

ALIGNMENTS

RESULT 1

AY417102

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

AY417102 Homo sapiens HCM6112 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
AY417102.1 GI:39773062
GSS.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1377)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1377)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission

gene	<1..>1377 /Locus_tag="HCM6112"
ORIGIN	
Query Match	71.8%; Score 1314; DB 29; Length 1377;
Best Local Similarity	95.6%; Pred. No. 2e-280;
Matches 1317; Conservative	0; Mismatches 60; Indels 0; Gaps 0;
QY	126 ATGGCTTGGGCAAGTAGGTAGGCTGGGCTCGTCGTGGCACTGCTGCTSCCCGTGGTGGTGCC 185
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Ddb	61 TCCAGCCAGGCACCGTGTGCGACTCACACAGGCGAGCATTTGAGCTTAGTGTCGAAAT 120
QY	246 GGGAAGGCCCTCTCCAGGGGCCCTTGCAAGGTCACGTGCTCCCTCATTTCTCGACTGGAGT 305
Ddb	121 GGGAAGGCCCTCTCCAGGGGCCCTTGCAAGGTCACGTGCTCCCTCATTTCTCGACTGGAGT 180
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Ddb	181 GGAGAGCGCTTCAGCCCCANNNGATCCGATNNNGAATGTCCATGTGCCCOCCTCCAC 240
QY	366 CTGAAATTCAATTGCTGGTTTCGGAGTGGCCTGCTGGCAGCAGCTAAATTTTACTTTCAAG 425
Ddb	241 CTGAAATTCAATTGCTGGTTTCGGAGTGGCCTGCTGGCAGCAGCTAAATTTTACTTTAAG 300
QY	426 GTCTTTTCGGCCCCAGACCCCTGAGAGCTGAGCGCTGCTGTGGAACTGCTGGCTCACACC 485
Ddb	301 GTCTTTTCGNNNNNNNNNNNNNGAGCTGACGCTGCTGTGGAATCTGCTGGCTGACACC 360
QY	486 CGCGTGACCAGAGCTCCATCAGGACCCCTGTGGTCAGCATCTCTGCTGCTCTTTATTTC 545
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Ddb	421 TCGGGCCAGCCHACAGATTGATGCGAGCTAACAGCACCTCCACACGGCTGCTGGTCCG 480
QY	606 GTCCAGAGCACATTAAGCTGTCTTGAGTAAACAAGCTGTGCTGAGCATCTCCAACTCG 665
Ddb	481 GTCCNNNAGCACATTAAGCTGTCTTGAGTAAACAAGNNNNNNNNNAGCATCTCCAACTCG 540
QY	666 GTCCAGGGTGCAATGTCCACCTGGGCACTTAATTGGGCTCAAACCGGTGGGTCTGTAG 725
Ddb	541 GTCCAGGNNNCANNTCCACCTGGGCACTTAATTGGGCTCAAACCGGTGGGTCTGTAG 600
QY	726 TCCCATGTCGCTATTTCATGTGTGATGTCACCATGTGTACAGTGAATATTCCTGCTG 785
Ddb	601 TCCCATGTCGCTATTTCATGTGTGATGTCACCATGTGTACAGTGAATATTCCTGCTG 660
QY	786 GAAGTCAATGCTCTCTCTTCCTGCTGGGCAACCCCATCATCTGCGCCACGAGATGCCACC 845
Ddb	661 GAAGTCAATNNNNNNNNNNNNCTGTGGGCAAGCCCATCATNNTGCACGAGATGCCACC 720
QY	846 CCTTTTGTGTGCCAAGGCATGTGGGTACCGAGGGCTCCATGTGCCACACCGTGGGCTCTCC 905
Ddb	721 CCTTTTGTGTGCCAAGGCATGTGGGTACCGAGGGCTCCATGTGCCACACCGTGGGCTCTCC 780
QY	906 CAGCAGCTGTTTGACTCTGGGCTCTCTGCTGTGCAAGAGCGCGGTGCCCTCAACCTGGAC 965
Ddb	781 CAGCAGCTGTTTGACTCTGGGCTCTCTGCTGTGCAAGAGCGCGGTGCCCTCAACCTGGAC 840
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Ddb	841 ATCACAGGGGAGCTGAGGTGGATGACAACTGCTGAACACTCTGCTCTGGGCGGGCTC 900
QY	1026 ATCCCGGAGGTGGCCCGCAGTTTCCCGAGGCCCATGCTGTGGTGTCTCAAAGGTGCGGCTG 1085
Ddb	901 ATCCCGGAGGTGGCCCGCAGTTTCCCGAGGCCCATGCTGTGGTGTCTCAAAGGTGCGGCTG 960
QY	1086 GGTGCCACACTGTGGGCATGCTCCACACAAAACAACGCCACCTGTGGGCTGAGCCCTTC 1145

961	Db	GGTGCACACCTGTGGCCATGTCCACAAACAGCCACCCCTGGCGTGCAGCCCTTC	1020
1146	Qy	GTGGAGGTCCTGGCCACAGCTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTGGATG	1205
1021	Db	GTGGAGGTCCTGGCCACAGCTCCAACTCGGCTTTCCATCCCTCTTCTCCCTGGATG	1080
1206	Qy	GTAGTCAACTTGAGACTCCAGCTCTCTGTGTCCAAAGTGAAGCTTCAGGGGACCACTT	1265
1081	Db	GTAGTGAACTTGAGACTCCAGCTCTCTGTGTCCAAAGTGAAGCTTCAGGGGACCACTT	1140
1266	Qy	GTGCTGGGGGATGTCCAGCTCACGGTGGGCTCTCTCCAAAGTGGGCTTCATTTGATCAGAT	1325
1141	Db	GTGCTGGGGGATGTCCAGCTCACAGTGGGCTCTCTCCAAAGTGGGCTTCATTTGATCAGAT	1200
1326	Qy	CAGGTGGCACACTGATGGGCACCGTTTTTGAAAGCCCTCTGTGAGACATCTCAATGCT	1385
1201	Db	CAGGTGGCACACTGATGGGCACCGTTTTTGAAAGCCCTCTGTGAGACATCTCAATGCT	1260
1386	Qy	CTCTTGGCCATGGGAATTCGCCCTCCCTGGTGTGGTCAACTTCACTATGTGGCCCTGAG	1445
1261	Db	CTCTTGGCCATGGGAATTCGCCCTCCCTGGTGTGGTCAACCTTCACTATGTGGCCCTGAG	1320
1446	Qy	ATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAAGACTGA	1502
1321	Db	ATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAAGACTGA	1377

RESULT 3	AK009619	1703 bp	mRNA	linear	HTC 20-SEP-2003
LOCUS	AK009619				
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310034f21 product:hypothetical lipid-binding serum glycoprotein containing protein, full insert sequence.				
ACCESSION	AK009619	GI:12844522			
VERSION	AK009619.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999).				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
TITLE	Genome Res. 10 (10), 1617-1630 (2000)				
JOURNAL	20499374				
MEDLINE	20499374				
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REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
AUTHORS	OKazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
AUTHORS	Functional annotation of a full-length mouse cDNA collection				
TITLE	Nature 409, 685-690 (2001)				
JOURNAL					

[illegible]

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5	REFERENCE	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
	AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
	TITLE	Nature 420, 563-573 (2002)
	JOURNAL	(bases 1 to 1696)
	REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
	AUTHORS	

6 (pages 1 to 1696).
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ADACHI, J., AIZAWA, K., AKAHIRA, S., AKIMURA, T., ARAI, A., AONO, H.,
AKRAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y.,
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TEJIMA, Y., TOYA, T., YAMAMURA, T., YASUNISHI, A., YOSHIDA, K.,
YOSHIDA, M., YOSHIMIZU, M. and HAYASHIZAKI, Y.

TITLE
JOURNAL
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAAGATCTCGAGTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, Y. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sueni-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://phantom.gsc.riken.go.jp/>

FEATURES
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Best Local Similarity 76.8%; Pred. No. 1.2e-181;
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 1253 CCACCTCCCAAGTGGCTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312
 QY |||||
 1354 TTGAGAAGCCCTGCTGGACCACTCTCAATGCTCTCTTGGCCATGGAATGCGCTGCTG 1413
 DB |||||
 1313 TCCAGAACCCCTGCTGGATCACTCAATGCTCTCTGCGGCGATGGGGTGTCTCTCCCA 1372
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 1414 GTGTGCTCACTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1473
 DB |||||
 1373 GGGTCACCAATTTACATTTATGCTCCACTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTG 1432
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 DB |||||
 1433 TATCCAGTGAAGTCTTCTACCAAGTGGAGCAAGACCAC 1472

RESULT 8
 Locus AK010130
 DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310069G19 product:hypothetical lipid-binding serum glycoprotein containing protein, full insert sequence.
 ACCESSION AK010130.1 GI:12845357
 VERSION 1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 Carninci, P. and Hayashizaki, Y.
 2 High efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
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Db TCACTATCTCTGATTTTCATGGATCCAGTGGGAGGTCCTCAGTCTACCAAGGTTTCAGA 278
QY TCTGTGATGTCCTGATGTCCTGCGCTCCACCTCGAAATTCATGCTGTGTTTCGAGTGGGCC 396
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Db ATCCAGTGGATCTTCTACAGAGCTGAGGCAAGACAC 1456

RESULT 9

AK010215

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

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JOURNAL

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AUTHORS

AK010215 1693 bp mRNA linear HTC 20-SEP-2003
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310079F.1 product:hypothetical Lipid-binding serum
glycoprotein containing protein, full insert sequence.

AK010215 1 GI:12845493
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5'-GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. Second
 strand cDNA was prepared with the primer adapter of sequence [5'
 GAGAGAGAGCTCTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved
 with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
 Host: SOUR.

FEATURES

source

Location/Qualifiers

1..1693
 /organism="Mus musculus"
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 /strain="C57BL/6J"
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 InterPro)
 putative"
 1676..1681
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 1693
 /note="putative"

misc_feature

polyA_signal

polyA_site

ORIGIN

Query Match 46.7%; Score 854.4; DB 11; Length 1693;
 Best Local Similarity 77.1%; Pred. No. 1.9e-178;
 Matches 1095; Conservative 0; Mismatches 311; Indels 14; Gaps 4;
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 53 GTGAGCAGCTGGGAGCAGCAGTGGCTAGGCAATGAGCTAGGCTGTCTGTCTGTGT 112
 166 TGCTSC-----CCGTGTGTGTGTCTCCAGCCAGGACCGTGTGCGACTCAACA 216
 113 TGCTGTCTGTGGGACTGTAGTCACTGTCTCTTGCCTGTCAATGTGTGCTCCGACTCA 172
 217 AGGAGCAGTTGAGCTAGCTGTGTAATTTGGAAAGAGCCCTCTCCAGGGCCCTGCGAG 276
 173 AGGAGCAGTTGAGTTATGTGTGGACATTTGGAAAGAGCCCTCTCCAGGGCCCTGCGAG 232
 277 TCACGTCCCTCATTTCTTGGACTGGAGTGGAGAGCGCTTCAGCCCAACAGATCCCGA 336
 233 TCACATATCTGTGATTTCAATGATCCAGTGGGAGGCTCTTCAGTCTACAGGGTTGAGA 292
 337 TTCTGAATGTCCATGTGCCCCGCCCTCCACCTGAAATTCATTTGCGGTTTCGGAGTGC 396
 293 TTCGGATGCCACGTGGCCCTTCTTCTACTTGAAGTTCATTTGCTGTGTTTGGGGTAC 352
 397 TGCTGGAGAGCTGAATTTTACTTTTCAAGGCTTTTCGCGCCCCAGAGGCCCTTGGAG 456

353 TATCAGCGCGCAGCCCAATTTACCATCAAAAGTCTTTAGTGTCCCGAGAGCCCATGGAGCTGG 412
 457 CGTGCCTGTGTGAAGTCTGTGGCTGTGACACCGCGGTGACCCAGAGCTCCATCAGAGACCCCTTG 516
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 517 TGGTCAGCATCTCTGCCCTGTCTTTATTTCTGGGGCCACGCCAACCAAGTTTGTATGGCAGTA 576
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 577 ACAGCAGCTCCACCGGCTGTGGTCTGTGTCGAGAGCAATTAAGCTGTCTTGAAGTA 636
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 1371 GGGTGACAACTACATATTATGTCCACTCTGAGGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1430
 1474 TATCCAGTGGGCTCTTCTTACAGAGCTGAGCAAGACAC 1513
 1431 TATCCAGTGGGCTTGTGCTTACCAGCACTGAGCCAGAACCA 1470

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Db	519	TCAGTACTCCCAAGAGCTGCTCGACGGGTGCAGAGGACATCAAGCTGACTAAACA	578
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RESULT 11

AK010157

LOCUS

DEFINITION

AKO:0157 1727 bp mRNA linear HTC 20-SEP-2003
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310074O15 product:hypothetical lipid-binding serum
glycoprotein containing protein, full insert sequence.

ACCESSION	
VERSION	
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SOURCE	
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REFERENCE	
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AUTHORS	
TITLE	
JOURNAL	
COMMENT	

AK010157
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20495374
11042159
3 Kono, H., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Matsui, K.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-699 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1727)
Adachi, J., Aizawa, K., Akahira, K., Akahira, T., Arai, A., Aono, H.,
Adachi, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2004, 10:59:00 ; Search time 49 Seconds
(without alignments)
2642.429 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265

Sequence: 1 MAWASRLGILLALLFPVGA.....PEIFVYGYVSSGLFYQS 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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17: /cgn2_6/prodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2265	100.0	458	9	US-09-965-529-28
2	2265	100.0	458	10	US-09-969-680A-28
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18	2260	99.8	458	12	US-10-180-550-498	Sequence 498, App
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ALIGNMENTS

RESULT 1
US-09-965-529-28
? Sequence 28, Application US/09965529
? Publication No. US20020182671A1
? GENERAL INFORMATION:
? APPLICANT: LAL, Preeti
? APPLICANT: YUE, Henry
? APPLICANT: TANG, Y. Tom
? APPLICANT: BANDMAN, Olga
? APPLICANT: BURFORD, Neil
? APPLICANT: AZIMZAI, Valda
? APPLICANT: BAUGHN, Mariah R.
? APPLICANT: LO, Dyrung Aina M.
? APPLICANT: PATTERSON, Chandra
? TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
? FILE REFERENCE: PF-0731 USA
? CURRENT APPLICATION NUMBER: US/09/965,529
? CURRENT FILING DATE: 2001-09-26
? PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US02/22315
? PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
? NUMBER OF SEQ ID NOS: 74
? SOFTWARE: PERL Program
? SEQ ID NO 28
? LENGTH: 458
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? OTHER INFORMATION: Incyte ID No. US20020182671A1 339343CD1
US-09-965-529-28

Query Match 100.0%; Score 2265; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 3e-209;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAWASRLGILLALLFPVGA...TGTVTTLNKAALSYVSEIGKAPLQALQVTVPHLDWS 60

QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELETLFPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELETLFPVELLADT 120
QY 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
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QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLLGKPIILPTDAT 240
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DB 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458

RESULT 2

US-09-969-680A-28
; Sequence 28, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZEMZAI, Yalda
; APPLICANT: BAUGHN, Maria R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 3393430CD1
US-09-969-680A-28

Query Match 100.0%; Score 2265; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 3e-209;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELETLFPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELETLFPVELLADT 120

QY 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
DB 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLLGKPIILPTDAT 240
DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLLGKPIILPTDAT 240
QY 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNNLNTSALGRL 300
DB 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNNLNTSALGRL 300
QY 301 IPEVARQFPEPMPVLLKVRIGATPVAMLHTNNATLRLOPPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQFPEPMPVLLKVRIGATPVAMLHTNNATLRLOPPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVKGQTTSVLGDVQLTVASSNVGFIIDQVRLTGMGTVEKPELIDHNA 420
DB 361 VVNLRLQLSVSKVKGQTTSVLGDVQLTVASSNVGFIIDQVRLTGMGTVEKPELIDHNA 420
QY 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458
DB 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458

RESULT 3

US-10-291-265-350
; Sequence 350, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 350
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-350

Query Match 100.0%; Score 2265; DB 15; Length 458;
Best Local Similarity 100.0%; Pred. No. 3e-209;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELETLFPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELETLFPVELLADT 120
QY 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
DB 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLLGKPIILPTDAT 240
DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLLGKPIILPTDAT 240
QY 241 PFVLPVRHVTGSGMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNNLNTSALGRL 300

Db 241 PFVLPVRHVTGSGMATVGLSQLPFSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATRLQPFVEVLATASNAFQSLFSLDV 360
Db 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATRLQPFVEVLATASNAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVQLQGTTSVLGQVLTIVASSNVGFIDTDQVRLTMGTVPFEKPLDLHLNA 420
Db 361 VVNLRLQLSVSKVQLQGTTSVLGQVLTIVASSNVGFIDTDQVRLTMGTVPFEKPLDLHLNA 420
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 4
US-10-291-265-822
; Sequence 822, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tag et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (795)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-822

Query Match 100.0%; Score 2265; DB 15; Length 458;
Best Local Similarity 100.0%; Pred. No. 3e-209;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60
Db 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60
QY 61 GEALQPTIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120
Db 61 GEALQPTIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120
QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVLYQKHIVKAVLSNKLCLISNL 180
Db 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVLYQKHIVKAVLSNKLCLISNL 180
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVSDYISLEVNVLFLGKPIILPTDAT 240
Db 181 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVSDYISLEVNVLFLGKPIILPTDAT 240
QY 241 PFVLPVRHVTGSGMATVGLSQLPFSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
Db 241 PFVLPVRHVTGSGMATVGLSQLPFSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATRLQPFVEVLATASNAFQSLFSLDV 360
Db 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNNATRLQPFVEVLATASNAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVQLQGTTSVLGQVLTIVASSNVGFIDTDQVRLTMGTVPFEKPLDLHLNA 420

Db 361 VVNLRLQLSVSKVQLQGTTSVLGQVLTIVASSNVGFIDTDQVRLTMGTVPFEKPLDLHLNA 420
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 5
US-10-206-915-498
; Sequence 498, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60
Db 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60
QY 61 GEALQPTIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120
Db 61 GEALQPTIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120
QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVLYQKHIVKAVLSNKLCLISNL 180
Db 121 RVTQSSIRTPVVISACSLFSGHANEFDCSNSTSHALLVLYQKHIVKAVLSNKLCLISNL 180
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVSDYISLEVNVLFLGKPIILPTDAT 240

Db 181 VQGVNHLGLLGLNPGVSGQIRYSWVSPTVTSYISLEVNNAVFLGLGNPIILFTDAT 240
QY 241 PFVLPRHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
Db 241 PFVLPREHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
Db 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVQLGTTSLVGLDVQVLTASSNVGFIIDTQVRLTGMGTVEKPLDLHNA 420
Db 361 VVNLRLQLSVSKVQLGTTSLVGLDVQVLTASSNVGFIIDTQVRLTGMGTVEKPLDLHNA 420
QY 421 LLAMGIALPGVVNLHYVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 6

US-10-199-670-498
; Sequence 498, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-199-670-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Freq. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLPWVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
Db 1 MAWASRLGLLLALLPWVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
QY 61 GZALQPTRIRIILNVHVRHLKPIAGFGVRLILAAANFTPKVFRAPPELETLTPVELLIADT 120
Db 61 GZALQPTRIRIILNVHVRHLKPIAGFGVRLILAAANFTPKVFRAPPELETLTPVELLIADT 120
QY 121 RVQSSIRTPVYSISACSLFSGHANEFDSNSTSHALLVLVOKHIAVLSNK-CLISISNL 180
Db 121 RVQSSIRTPVYSISACSLFSGHANEFDSNSTSHALLVLVOKHIAVLSNK-CLISISNL 180
QY 181 VQGVNHLGLLGLNPGVSGQIRYSWVSPTVTSYISLEVNNAVFLGLGNPIILFTDAT 240
Db 181 VQGVNHLGLLGLNPGVSGQIRYSWVSPTVTSYISLEVNNAVFLGLGNPIILFTDAT 240
QY 241 PFVLPRHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
Db 241 PFVLPRHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
Db 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVQLGTTSLVGLDVQVLTASSNVGFIIDTQVRLTGMGTVEKPLDLHNA 420
Db 361 VVNLRLQLSVSKVQLGTTSLVGLDVQVLTASSNVGFIIDTQVRLTGMGTVEKPLDLHNA 420
QY 421 LLAMGIALPGVVNLHYVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 7

US-10-201-858-498
; Sequence 498, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544

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; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-498

Query Match          99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGALLALLPVVGASTPGTWRINKAALSVSSEIGKAPLQALQVTVPEFLDWS 60
Db 1 MAWASRLGALLALLPVVGASTPGTWRINKAALSVSSEIGKAPLQALQVTVPEFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
Db 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
QY 121 RVTOSSIRTPVVISACSLFSGHANEFQGSNSTSHALLVWQKHKAVLSNKLCLISNKL 180
Db 121 RVTOSSIRTPVVISACSLFSGHANEFQGSNSTSHALLVWQKHKAVLSNKLCLISNKL 180
QY 181 VQGVNVHGLTILGLNPVGPESQIRYSMSVPTVTSYISLEVNNAVLFLLGKPIILLPTDAT 240
Db 181 VQGVNVHGLTILGLNPVGPESQIRYSMSVPTVTSYISLEVNNAVLFLLGKPIILLPTDAT 240
QY 241 PFVLPVRHVTGSGMATVGSQOLFPSALLLQKAGALNDITQGRSDNCLNLTSGALGRL 300
Db 241 PFVLPVRHVTGSGMATVGSQOLFPSALLLQKAGALNDITQGRSDNCLNLTSGALGRL 300
QY 301 IPEVARQPEBPMPVVLKVLGATPVAMLHTNATLROPEVEVLATASNAFQSLFSLDV 360
Db 301 IPEVARQPEBPMPVVLKVLGATPVAMLHTNATLROPEVEVLATASNAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVKLQGTTSVLGQVAVSSNVGFIIDTQVRLTGMVTFEKLPHLHNA 420
Db 361 VVNLRLQLSVSKVKLQGTTSVLGQVAVSSNVGFIIDTQVRLTGMVTFEKLPHLHNA 420
QY 421 LLANGIALPGVNVHLHYVAPEIFVVEGYVVSGLFPYQS 458
Db 421 LLANGIALPGVNVHLHYVAPEIFVVEGYVVSGLFPYQS 458

RESULT 8
US-10-081-056-322
; Sequence 322, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC1
; CURRENT APPLICATION NUMBER: US/10/081.056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
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; PRIOR APPLICATION NUMBER: PCT/US01/00000
 ; PRIOR FILING DATE: 2001-06-28
 ; NUMBER OF SEQ ID NOS: 383
 ; SEQ ID NO 322
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Homosapiens
 US-10-081-056-322

Query Match 99.8%; Score 2260; DB 12; Length 458;
 Best Local Similarity 99.8%; Pred. No. 9.2e-209;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTPHFLDWS 60
 Db 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTPHFLDWS 60
 QY 61 GEALQPTRIRILNVHVRHLKFIAGVGRLLAAANFTKVFRAPELELTLPVELLADT 120
 Db 61 GEALQPTRIRILNVHVRHLKFIAGVGRLLAAANFTKVFRAPELELTLPVELLADT 120
 QY 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHIAVLSNKLCLISNL 180
 Db 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHIAVLSNKLCLISNL 180
 QY 181 VQGVNHLGLTGLNPGVPSQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
 Db 181 VQGVNHLGLTGLNPGVPSQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
 QY 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQGLSDNLLNTSALGRL 300
 Db 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQGLSDNLLNTSALGRL 300
 QY 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNATLRLQPPVEVLATASNSAFQSLFSLDV 360
 Db 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNATLRLQPPVEVLATASNSAFQSLFSLDV 360
 QY 361 VVNLRLQLSVSKVKGTTSLVGDVQVLTVAASNVGFDITDQVRLMGTVFEKPLDLHNA 420
 Db 361 VVNLRLQLSVSKVKGTTSLVGDVQVLTVAASNVGFDITDQVRLMGTVFEKPLDLHNA 420
 QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458
 Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 9

US-10-205-890-498
 ; Sequence 498, Application US/10205890
 ; Publication No. US20040048334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430RIC519
 ; CURRENT APPLICATION NUMBER: US/10/205,890
 ; PRIOR FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 63/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 498
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-205-890-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
 Best Local Similarity 99.8%; Pred. No. 9.2e-209;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTPHFLDWS 60
 Db 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTPHFLDWS 60
 QY 61 GEALQPTRIRILNVHVRHLKFIAGVGRLLAAANFTKVFRAPELELTLPVELLADT 120
 Db 61 GEALQPTRIRILNVHVRHLKFIAGVGRLLAAANFTKVFRAPELELTLPVELLADT 120
 QY 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHIAVLSNKLCLISNL 180
 Db 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHIAVLSNKLCLISNL 180
 QY 181 VQGVNHLGLTGLNPGVPSQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
 Db 181 VQGVNHLGLTGLNPGVPSQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
 QY 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQGLSDNLLNTSALGRL 300
 Db 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQGLSDNLLNTSALGRL 300
 QY 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNATLRLQPPVEVLATASNSAFQSLFSLDV 360
 Db 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNATLRLQPPVEVLATASNSAFQSLFSLDV 360
 QY 361 VVNLRLQLSVSKVKGTTSLVGDVQVLTVAASNVGFDITDQVRLMGTVFEKPLDLHNA 420
 Db 361 VVNLRLQLSVSKVKGTTSLVGDVQVLTVAASNVGFDITDQVRLMGTVFEKPLDLHNA 420
 QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458
 Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 10

US-10-208-024-498
 ; Sequence 498, Application US/10208024
 ; Publication No. US20040048335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.

APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C538
CURRENT APPLICATION NUMBER: US/10/208,024
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 498
LENGTH: 458
TYPE: PRT
ORGANISM: Homo Sapien
US-10-208-024-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAWASRLGILLALLPVVGASTPGTVVRLNKAALSVSEIGKAPLQALQVTPHFLDWS 60
DB 1 MAWASRLGILLALLPVVGASTPGTVVRLNKAALSVSEIGKAPLQALQVTPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPELTLPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPELTLPVELLADT 120
QY 121 RVTQSSIRTPVVISIACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISINL 180
DB 121 RVTQSSIRTPVVISIACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISINL 180
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVSPVTVSDYISLEVNVLFLGKPIILPTDAT 240
DB 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVSPVTVSDYISLEVNVLFLGKPIILPTDAT 240
QY 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQSRDNLNLTALGRL 300
DB 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQSRDNLNLTALGRL 300
QY 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNATLRLQPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNATLRLQPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSVSKVQLGTTSLVGLDVLTVASSNVGFIDTQVRLMGTVFEXPLDLHNA 420
DB 361 VVNLRLQLSVSKVQLGTTSLVGLDVLTVASSNVGFIDTQVRLMGTVFEXPLDLHNA 420
QY 421 LLAMGIALPGVNLHYVAPEIFVVEGYVVISGGLFYQS 458
DB 421 LLAMGIALPGVNLHYVAPEIFVVEGYVVISGGLFYQS 458

RESULT 11

US-10-201-853-498
Sequence 498, Application US/10201853
Publication No. US20040053358A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C465
CURRENT APPLICATION NUMBER: US/10/201,853
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 498
LENGTH: 458
TYPE: PRT
ORGANISM: Homo Sapien
US-10-201-853-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAWASRLGILLALLPVVGASTPGTVVRLNKAALSVSEIGKAPLQALQVTPHFLDWS 60
DB 1 MAWASRLGILLALLPVVGASTPGTVVRLNKAALSVSEIGKAPLQALQVTPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPELTLPVELLADT 120
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPELTLPVELLADT 120
QY 121 RVTQSSIRTPVVISIACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISINL 180
DB 121 RVTQSSIRTPVVISIACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISINL 180
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVSPVTVSDYISLEVNVLFLGKPIILPTDAT 240
DB 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVSPVTVSDYISLEVNVLFLGKPIILPTDAT 240
QY 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQSRDNLNLTALGRL 300
DB 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQSRDNLNLTALGRL 300
QY 301 IPEVARQPEPMPVVLKVRLGATPVAMLHTNATLRLQPFVEVLATASNSAFQSLFSLDV 360

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Db 301 IPVAQFPEFWLKVRLGATPVAMLHTNATLRQPFVEVLATASAFOSLFLSDV 360
QY 361 VVNLRLQLSVKVKLQTTSVLGDVQLTVASSNVGFIDTQVRLMGTVFEKPLDLHNA 420
Db 361 VVNLRLQLSVKVKLQTTSVLGDVQLTVASSNVGFIDTQVRLMGTVFEKPLDLHNA 420
QY 421 LLAMGIALPGVNLHYVAPFIYEGVWVSSGLFYQS 458
Db 421 LLAMGIALPGVNLHYVAPFIYEGVWVSSGLFYQS 458

RESULT 12
US-10-174-581-498
? Sequence 498, Application US/10174581
? Publication No. US20030017540A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Chen, Jian
? APPLICANT: Destoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Garney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3430R1C41
? CURRENT APPLICATION NUMBER: US/10/174,581
? CURRENT FILING DATE: 2002-06-18
? PRIOR APPLICATION NUMBER: 10/052586
? PRIOR FILING DATE: 2002-01-15
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059266
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063120
? PRIOR FILING DATE: 1997-10-24
? PRIOR APPLICATION NUMBER: 60/063121
? PRIOR FILING DATE: 1997-10-24
? PRIOR APPLICATION NUMBER: 60/063486
? PRIOR FILING DATE: 1997-10-21
? PRIOR APPLICATION NUMBER: 60/063540
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/063541
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/063544
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/063564
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/063734
? PRIOR FILING DATE: 1997-10-29
? PRIOR APPLICATION NUMBER: 60/063870
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/065311
? PRIOR FILING DATE: 1997-11-13
? PRIOR APPLICATION NUMBER: 60/066120
? PRIOR FILING DATE: 1997-11-21
? PRIOR APPLICATION NUMBER: 60/066466
? PRIOR FILING DATE: 1997-11-24
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? PRIOR FILING DATE: 1997-11-24
? PRIOR APPLICATION NUMBER: 60/069335
? PRIOR FILING DATE: 1997-12-11
? PRIOR APPLICATION NUMBER: 60/069425
? PRIOR FILING DATE: 1997-12-12
? PRIOR APPLICATION NUMBER: 60/069870
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/068017
? PRIOR FILING DATE: 1997-12-18
? PRIOR APPLICATION NUMBER: 60/077450
? PRIOR FILING DATE: 1998-03-10
? PRIOR APPLICATION NUMBER: 60/077632
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077649
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/078886
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/078939
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079664
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? PRIOR FILING DATE: 1998-03-31
? PRIOR APPLICATION NUMBER: 60/080327
? PRIOR FILING DATE: 1998-04-01
? PRIOR APPLICATION NUMBER: 60/080333
? PRIOR FILING DATE: 1998-04-01
? PRIOR APPLICATION NUMBER: 60/081049
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? PRIOR FILING DATE: 1998-04-08
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? PRIOR FILING DATE: 1998-04-09
? PRIOR APPLICATION NUMBER: 60/081838
? PRIOR FILING DATE: 1998-04-15
? PRIOR APPLICATION NUMBER: 60/082568
? PRIOR FILING DATE: 1998-04-21
? PRIOR APPLICATION NUMBER: 60/082569
? PRIOR FILING DATE: 1998-04-21
? PRIOR APPLICATION NUMBER: 60/082704
? PRIOR FILING DATE: 1998-04-22
? PRIOR APPLICATION NUMBER: 60/082797
? PRIOR FILING DATE: 1998-04-22
? PRIOR APPLICATION NUMBER: 60/083322
? PRIOR FILING DATE: 1998-04-28
? PRIOR APPLICATION NUMBER: 60/083495
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? PRIOR APPLICATION NUMBER: 60/083496
? PRIOR FILING DATE: 1998-04-29
? PRIOR APPLICATION NUMBER: 60/083499
? PRIOR FILING DATE: 1998-04-29
? PRIOR APPLICATION NUMBER: 60/083559
? PRIOR FILING DATE: 1998-04-29
? PRIOR APPLICATION NUMBER: 60/084366
? PRIOR FILING DATE: 1998-05-05
? PRIOR APPLICATION NUMBER: 60/084414
? PRIOR FILING DATE: 1998-05-06
? PRIOR APPLICATION NUMBER: 60/084639
? PRIOR FILING DATE: 1998-05-07
? PRIOR APPLICATION NUMBER: 60/084640
? PRIOR FILING DATE: 1998-05-07
? PRIOR APPLICATION NUMBER: 60/084643
? PRIOR FILING DATE: 1998-05-07
? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085579
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085580
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085582
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085700
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/086023
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; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/086392
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/086486
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087098
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087208
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087609
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087827
 ; PRIOR FILING DATE: 1998-06-03
 ; PRIOR APPLICATION NUMBER: 60/088025
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088028
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088029
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088033
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088167
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088202
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088212
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088217
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088326
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088655
 ; PRIOR FILING DATE: 1998-06-09
 ; PRIOR APPLICATION NUMBER: 60/088722
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088738
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088740
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088811
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088824
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088825
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088826
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088861
 ; PRIOR FILING DATE: 1998-06-11
 ; PRIOR APPLICATION NUMBER: 60/088863
 ; PRIOR FILING DATE: 1998-06-11
 ; PRIOR APPLICATION NUMBER: 60/088876
 ; PRIOR FILING DATE: 1998-06-11
 ; PRIOR APPLICATION NUMBER: 60/089090
 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: 60/089105
 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: 60/089512
 ; PRIOR FILING DATE: 1998-06-15
 ; PRIOR APPLICATION NUMBER: 60/089514
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653

Query Match 99.8%; Score 2260; DB 12; Length 458;
 Best Local Similarity 99.8%; Pred. No. 9.2e-209;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHLWDS 60
 DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHLWDS 60
 QY 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
 DB 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
 QY 121 RVTQSSIRTPVWSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISINL 180
 DB 121 RVTQSSIRTPVWSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISINL 180
 QY 181 VQGVNHLGLTLGLNPGVPSQIRYSVSVTVTSYISLEVNVLFLGPNPILPTDAT 240
 DB 181 VQGVNHLGLTLGLNPGVPSQIRYSVSVTVTSYISLEVNVLFLGPNPILPTDAT 240
 QY 241 PFVLPRHVGTGEGMATVGLSQOLFDSALLLQKAGALNCDITGOLRSDDNLLNTSALGRL 300
 DB 241 PFVLPRHVGTGEGMATVGLSQOLFDSALLLQKAGALNCDITGOLRSDDNLLNTSALGRL 300
 QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPFVEVLATASNSAFQSLFSLDV 360
 DB 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPFVEVLATASNSAFQSLFSLDV 360
 QY 361 VVNLRLQLSYKVKLQGTTSVLGVDVQLTVASSNVGRIDTQVRLTMTGTVFEKPLLDHNA 420
 DB 361 VVNLRLQLSYKVKLQGTTSVLGVDVQLTVASSNVGRIDTQVRLTMTGTVFEKPLLDHNA 420
 QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVWISSGLFYQS 458
 DB 421 LLAMGIALPGVNLHYVAPEIFVYEGYVWISSGLFYQS 458

RESULT 13

US-10-176-483-498
 ; Sequence 498, Application US/10176483
 ; Publication No. US20030017541A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430RIC68
 ; CURRENT APPLICATION NUMBER: US/10/176,483
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 498
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien

US-10-176-483-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
 Best Local Similarity 99.8%; Pred. No. 9.2e-209;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHLWDS 60
 DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHLWDS 60
 QY 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
 DB 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120

QY 121 RVTQSSIRTPVVSISACSLFSGHANEDGNSNSTSHALLVLVQKHKAVLSNKLCLSISNL 180
DB 121 RVTQSSIRTPVVSISACSLFSGHANEDGNSNSTSHALLVLVQKHKAVLSNKLCLSISNL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
DB 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQFPPEMPVVLKVRIGATFVAMLTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQFPPEMPVVLKVRIGATFVAMLTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSYSKVKLQCTTSVLGDVQLTVAASNNGFIDTQVRLMGTVEKPLLDHNA 420
DB 361 VVNLRLQLSYSKVKLQCTTSVLGDVQLTVAASNNGFIDTQVRLMGTVEKPLLDHNA 420
QY 421 LLANGIALPGVNLHYVAPEIFVYGVVWISSGLFYQS 458
DB 421 LLANGIALPGVNLHYVAPEIFVYGVVWISSGLFYQS 458

RESULT 14

US-10-176-749-498
; Sequence 498, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVSSEIGKAPLQALQVTVPHFLDWS 60
DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVSSEIGKAPLQALQVTVPHFLDWS 60
QY 61 GEALQPTIRILNVHVPRLHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
DB 61 GEALQPTIRILNVHVPRLHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
QY 121 RVTQSSIRTPVVSISACSLFSGHANEDGNSNSTSHALLVLVQKHKAVLSNKLCLSISNL 180
DB 121 RVTQSSIRTPVVSISACSLFSGHANEDGNSNSTSHALLVLVQKHKAVLSNKLCLSISNL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240

DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
DB 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQFPPEMPVVLKVRIGATFVAMLTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQFPPEMPVVLKVRIGATFVAMLTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNLRLQLSYSKVKLQCTTSVLGDVQLTVAASNNGFIDTQVRLMGTVEKPLLDHNA 420
DB 361 VVNLRLQLSYSKVKLQCTTSVLGDVQLTVAASNNGFIDTQVRLMGTVEKPLLDHNA 420
QY 421 LLANGIALPGVNLHYVAPEIFVYGVVWISSGLFYQS 458
DB 421 LLANGIALPGVNLHYVAPEIFVYGVVWISSGLFYQS 458

RESULT 15

US-10-176-914-498
; Sequence 498, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-498

Query Match 99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVSSEIGKAPLQALQVTVPHFLDWS 60
DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVSSEIGKAPLQALQVTVPHFLDWS 60
QY 61 GEALQPTIRILNVHVPRLHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
DB 61 GEALQPTIRILNVHVPRLHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120
QY 121 RVTQSSIRTPVVSISACSLFSGHANEDGNSNSTSHALLVLVQKHKAVLSNKLCLSISNL 180
DB 121 RVTQSSIRTPVVSISACSLFSGHANEDGNSNSTSHALLVLVQKHKAVLSNKLCLSISNL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
DB 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
DB 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
QY 301 IPEVARQFPPEMPVVLKVRIGATFVAMLTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360

Db	301	IPVAVQFPEPMPVVKYRLGATPVAVLHTNATLRLQPEVEVLATASNAFQSLFSLDV	360
Qy	361	VVNRLQLSVSKYKLGQTTISVLGEVOLTWASSNVGFIDTDQVRLMGTVEKPLLDHNA	420
Db	361	VVNRLQLSVSKYKLGQTTISVLGEVOLTWASSNVGFIDTDQVRLMGTVEKPLLDHNA	420
Qy	421	LLANGIALPQVNLHYVAPEIFYEGYVWISSGLFYQS	458
Db	421	LLANG-ALPGVNLHYVAPEIFYEGYVWISSGLFYQS	458

Search completed: June 29, 2004, 11:02:31
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2004, 10:55:39 ; Search time 17 Seconds
(without alignments)
1402.831 Million cell updates/sec

Title: US-10-069-034-28
Perfect score: 2265
Sequence: 1 MAWASRLGLLALLPVVGA.....PEIFVGYGVVSSGLFQYS 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2258	99.7	458	1	BPI1_HUMAN
2	2489	95.7	462	1	BPI1_MOUSE
3	392.5	17.3	470	1	LPC4_RAT
4	386	17.0	477	1	LPC3_HUMAN
5	380	16.8	472	1	LPC3_MOUSE
6	358	15.8	575	1	LPC4_HUMAN
7	353	15.6	473	1	LPC3_RAT
8	330.3	14.6	507	1	BPL2_HUMAN
9	313.3	13.8	509	1	BPL2_MOUSE
10	306	13.5	453	1	BPL3_HUMAN
11	283	12.5	483	1	BPI_HUMAN
12	280	12.4	449	1	BPL3_MOUSE
13	259	11.4	481	1	LBP_HUMAN
14	257.5	11.4	481	1	LBP_MOUSE
15	251	11.1	482	1	LBP_RABIT
16	250	11.0	445	1	BPI_MOUSE
17	247.5	10.9	482	1	BPI_BOVIN
18	246.5	10.9	481	1	LBP_RAT
19	173	7.6	493	1	PLTP_MOUSE
20	159.5	7.0	493	1	PLTP_HUMAN
21	138.5	6.1	473	1	LPC1_BOVIN
22	131.5	5.8	428	1	LPC1_MOUSE
23	118.5	5.2	484	1	LPC1_HUMAN
24	112.5	5.0	2432	1	Y43R_IRV6
25	109	4.8	493	1	CETP_MACFA
26	103.5	4.6	581	1	LR15_HUMAN
27	103	4.5	488	1	Y41S_HAEN
28	102.5	4.5	1118	1	CARB_YEAST
29	101.5	4.5	637	1	NUSM_STRPU
30	100	4.4	1774	1	MSAS_PENPA
31	99.5	4.4	2067	1	NCOS_MOUSE
32	99	4.4	858	1	ATMA_ECOLI
33	99	4.4	1945	1	Z236_HUMAN

34	37.5	4.3	1181	1	ITA7_HUMAN
35	97	4.3	378	1	DP3B_STRPN
36	97	4.3	501	1	DLDH_PEA
37	96.5	4.3	378	1	DP3B_STRR6
38	96.5	4.3	529	1	VG_P_SV5
39	96.5	4.3	560	1	ATP2_NICPL
40	96.5	4.3	711	1	MMIA_STRCO
41	96	4.2	637	1	NPT2_RAT
42	96	4.2	2185	1	PKR1_DICDI
43	95.5	4.2	551	1	ATP2_ORISA
44	95	4.2	394	1	LPXB_SYNY3
45	95	4.2	760	1	SIX4_HUMAN

ALIGNMENTS

RESULT 1

ID	BPI1_HUMAN	STANDARD;	PRT;	458 AA.
AC	Q8N4F0; Q8NF07;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Bactericidal/permeability-increasing protein-like 1 precursor (Long			
DE	DE palate, lung and nasal epithelium carcinoma associated protein 2)			
DE	(RYSR)			
GN	BPI1L OR LPLUNC2 OR C20ORF184.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUR=Trachea;			
RX	MEDLINE=22172641; PubMed=12185532;			
RA	Mulero J.J., Boyle B.J., Bradley S., Bright J.M., Nelken S.T.,			
RA	Ho T.T., Mize N.K., Childs J.D., Ballinger D.G., Ford J.E., Rupp F.;			
ET	"Three new human members of the lipid transfer/lipoplysaccharide			
ET	binding protein family (LTP/LBP).";			
RL	Immunogenetics 54:293-300(2002).			
RP	SEQUENCE FROM N.A.			
RN	[2]			
RA	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Sagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,			
RA	Lehvasaaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marst V.L., Martin S.L., McConnachie L.J., McKay K., McMurray A.A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prachalingam S.R., Plumb R.M., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,			
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.N., Sycamore N., Taylor R., Tee L., Thomas D.M., Thorpe A.,			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			
RT	"The DNA sequence and comparative analysis of human chromosome 20.";			
RL	Nature 414:865-871(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			

RC RX TISSUE=Brain, Lung, and Testis;
 MEDLINE=22388257; PubMed=12477932;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausberger R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gattarone P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulys S.W.,
 RA Villalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahlberg J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalls D.E.,
 RA Schermerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Petal brain;
 RX MEDLINE=22721692; PubMed=12837268;
 RA Andraut J.-B., Gaillard I., Giorgi D., Rouquier S.;
 RT "Expansion of the BPI family by duplication on human chromosome 20:
 RT characterization of the RY gene cluster in 20q11.21 encoding olfactory
 RT transporters/antimicrobial-like peptides.";
 RL Genomics 82:172-184 (2003).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in tonsils, especially in
 CC hypertrophic tonsils. Detected at very low levels in fetal liver.
 CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
 CC family.
 CC
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 CC
 DR EMBL; AF465765; AA473983.1; -;
 DR EMBL; BC034415; AA434415.1; -;
 DR EMBL; AL121756; -; NOT ANNOTATED_CDS.
 DR Genew; HGNC:16177; BPI.L.
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
 DR SMART; SM00329; B2-2; 1.
 DR PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
 DR Signal.
 FT SIGNAL.
 FT CHAIN.
 FT 1 20 POTENTIAL.
 FT 21 458 BACTERICIDIAL/PERMEABILITY-INCREASING
 FT PROTEIN-LIKE 1.
 FT DOMAIN.
 FT 268 271 POLY-LEU.
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 458 AA; 49130 MW; FE647AV5CC2FA2AB CRC64;
 Query Match 99.7%; Score 2258; DB 1; Length 458;
 Best Local Similarity 99.8%; Pred. No. 5e-154;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 XAWASLGLHLLALLLPVVGASTGTGTVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
 DB 1 MAWASLGLHLLALLLPVVGASTGTGTVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
 QY 61 GEALQPTIRILNVVPRHLKFIAGVGVRLAAANFTKVFRAPELELTLPVELLADT 120

DB 61 GEALQPTIRILNVVPRHLKFIAGVGVRLAAANFTKVFRAPELELTLPVELLADT 120
 QY 121 RVTOSSTIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVOKHKAVLSNKLCLISNL 180
 DB 121 RVTOSSTIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVOKHKAVLSNKLCLISNL 180
 QY 181 VQGVNVHLGLTGLNPNVPSQIRYSVMVPTVTSVDSISLEWNAVLFGKPIILPTDAT 240
 DB 181 VQGVNVHLGLTGLNPNVPSQIRYSVMVPTVTSVDSISLEWNAVLFGKPIILPTDAT 240
 QY 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLOKAGALNLDITQGRSDNLLNTSALGRL 300
 DB 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLOKAGALNLDITQGRSDNLLNTSALGRL 300
 QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLTNNATLRLOPPFVVLATASNAFQSLFSLDV 360
 DB 301 IPEVARQFPPEMPVVLKVRIGATPVAMLTNNATLRLOPPFVVLATASNAFQSLFSLDV 360
 QY 361 VVNLRLQLSVSKVKLQCTTSVLGDVLTVAASNVGFTDQVPTLMCTVFEKPLLDHNA 420
 DB 361 VVNLRLQLSVSKVKLQCTTSVLGDVLTVAASNVGFTDQVPTLMCTVFEKPLLDHNA 420
 QY 421 LLAMGIALPGVNLHYVAPEIFVYEGVYVWISSGLFYQS 458
 DB 421 LLAMGIALPGVNLHYVAPEIFVYEGVYVWISSGLFYQS 458
 RESULT 2
 ID BPI.L MOUSE STANDARD; PRT; 462 AA.
 AC Q8C1E1; Q8BVZ0; Q8C1E2; Q9D713; Q9D744;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Bactericidal/permeability-increasing protein-like 1 precursor.
 GN BPI.L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE= Tongue;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaj H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verard L.G., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC
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CC
CC EMBL: AK009619; BAC26395.1; -
CC EMBL: AK009754; BAC26479.1; -
CC EMBL: AK028156; BAC25783.1; -
CC EMBL: AK028158; BAC25784.1; -
CC EMBL: AK075874; BAC36021.1; -
CC MGD; NGI:1913807; 231003421Rik.
CC InterPro: IPR001124; LBP_BPI_CETP.
CC Pfam: PF02886; LBP_BPI_CETP_C; 1.
CC SMART; SM00329; BP12; 1.
CC PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
CC SIGNAL.
CC CHAIN 1 22 POTENTIAL.
CC 23 462 BACTERICIDAL/PERMEABILITY-INCREASING
CC PROTEIN-LIKE 1.
CC FT CARBOHYD 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 73 Q -> H (IN REF. 1; BAC25783).
CC FT CONFLICT 108 P -> T (IN REF. 1; BAC25783).
CC FT CONFLICT 134 I -> A (IN REF. 1; BAC25783).
CC FT CONFLICT 143 I -> L (IN REF. 1; BAC26479).
CC FT CONFLICT 251 P -> L (IN REF. 1; BAC26395).
CC FT CONFLICT 422 T -> P (IN REF. 1; BAC36021).
CC FT CONFLICT 419 L -> V (IN REF. 1; BAC36021).
CC SEQUENCE 462 AA; 49521 MW; 5D4F6D1F2AD57F45 CRC64;
Query Match
Best Local Similarity 65.7%; Score 1489; DB 1; Length 462;
Matches 313; Conservative 49; Mismatches 95; Indels 4; Gaps 2;
QY 1 MAAWRIGLILALL---PVGASTPGTVEANKAALSYSVSGKAPLQAVTVEHPL 57
DB 1 MARACSLGLILLLLLRVTVTSLPVIIVRLNKALDYVSDIGKAPLQAVTISDFM 60
QY 58 DWSGEALPTRIILNVHPRHLKFIAGFGVRLAAANFTKVFRAPELELTLPVELL 117
DB 61 DPSGEVLOSTRVQILDAHVFFYLLKFIAGFGVHLGAAANFTIKFVSPEPMELVLPDIL 120
QY 118 ADTRVTSQSIPTPVVSIACSLFSGEANEFDGNSNSTSHALLVQKHKAVLSNKLCLSI 177
DB 121 ADWHVARDISGLTVLSPACSSIFSPAGMLDGSISTQELLDRVQEHKADLNKLCHV 180
QY 178 SNLVGVNHLGTLIGLNPVGPESQIRYSMSVPTVTSYISLEVNALVFLGKPIILPT 237
DB 181 YGLVQDLNVHLGTLIGLSPVGPESQIRYSITSMPTITSNYISLDIGAILSLGKPIILPM 240
QY 238 -DATEPFLVPRHVTGSGMATVGLSOOLEFSALELLLOKAGNLDITGQIRSDNLLNTSA 296
DB 241 HGAHEFVLPPWLDGADAGATVGLSOLHFEDCALMLQKAGSLNLEITGQINSKNNPLNTSV 300
QY 297 LGRLLPEVAROPPEPMPVVLKVLGATPVAMHTNNATRLQPFVEVLATANSASFQSLF 356
DB 301 LGQLIPEVAHLFPEPTPLVQLGATPVTLTNSNTLQQLPVEVFAAPSNAALQELF 360
QY 357 SLDVVNRLQLSVGKVLQGTTSVLGQVLTAVSSNVGFIITDQVRLTIMGVTFEKLPLD 416
DB 361 SLDVVNRLDLQSVSKAKLRGTSLSLGGFQLSVATNSVNGSVDMQVTLITSTVFQKPLD 420
QY 417 HLNALLANGIALPGVNLHLYAPFVYEGYVYVSSGLFYQ 457

Db 421 HLNALLCGVVLPRVNLHLYHSEVLVREGYVYVSSGLAYQ 461
RESULT 3
ID LPC4 RAT STANDARD; PRT; 470 AA.
AC Q05704;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Long palate, lung and nasal epithelium carcinoma associated protein 4
DE (Potential ligand-binding protein RY2G5) (Fragment).
GN L2LUNC4 OR RY2G5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Olfactory epithelium;
RC MEDLINE=92007724; PubMed=1915264;
RA Dear T.N., Boehm T., Reverte E.B., Rabbitts T.H.;
RT 'Novel genes for potential ligand-binding proteins in subregions of
RT the olfactory mucosa'.
RL EMBL J. 10:2813-2819 (1991).
CC -1- FUNCTION: May have the capacity of recognizing and binding
CC specific classes of odorants, may act as carrier molecules,
CC transporting odorants across the mucus layer to access the
CC receptor sites. May serve as a primary defense mechanism by
CC recognizing and removing potentially harmful odorants or
CC pathogenic microorganisms from the mucosa or clearing the excess
CC odorant from the mucus to enable new odorant stimuli to be
CC received. May bind polychlorinated biphenyls thereby protecting
CC lung epithelial cells from damage by such molecules.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in olfactory mucosa but
CC undetectable in thymus, kidney, lung, brain, spleen and liver.
CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X60660; CAA43067.1; -
CC InterPro; IPR001124; LBP_BPI_CETP.
CC Pfam; PF02886; LBP_BPI_CETP_C; 1.
CC SMART; SM00328; BP11; 1.
CC SMART; SM00329; BP12; 1.
CC PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
CC NON TER 1
CC DOMAIN 10 81 GLY-RICH.
CC CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 470 AA; 49593 MW; A4DF9403166AC926 CRC64;
Query Match
Best Local Similarity 17.3%; Score 392.5; DB 1; Length 470;
Matches 109; Conservative 81; Mismatches 182; Indels 33; Gaps 5;
QY 67 TRIRILNVHPRHLKFIAGFGVRLAAANFTKVFRAPELELTLPVELLADTRVTSQ 126
DB 80 TGLRIVELTFRVSVRLPGVGVLSLTRYVAINGKSLGFLDIAVEVNITAKVRLTMDR 139
QY 127 IRTPVVISACSLFSGH-----ANEFGNSNSTSHALLVQKHKAVLSNKLCLSI 176
DB 140 TGYPLVIERCTLLGGIKVLLRGLLELVN-----LVNRVLNVLPDLCP 189
QY 177 ISNLVQGVNHLGTLIGLNPVGPESQIRYSMSVPTVTSYISLEVNAL-----F 227

Db 190 VDVVLGVNQLGLVDSLVPLGLIGSVQYTFSSPLVTGFELELMTLVGEAGGLIDY 249

Qy 228 LLGKPIILPDTATPVLPRHVTGEGSMATVGLSQOLFDSALLQKAGALMDITGOLRS 287

Db 250 PLGREAMLPQPMELPPMGDNTNSQLA---ISANFSLSSVLTMLQKQALDIDITDGMFE 306

Qy 288 DDNLLNTSALGRLLPEVARQPEMPVVLKVRIGATPVAMHTNATRLQPPFVEVLATA 347

Db 307 DLPLATSTLIGALPKVFOQYPSREPLTIRIQVNPPTVTTLQDKALKVFPATSEVVVSQ 366

Qy 348 SNSAFQSLFSDVVNLRQLQSVSKVQLGTTSTVLGVQVLTVASSNGFDTDQVRLMG 407

Db 367 PNQVETICLIDVDVTLDAFSVEGDKLM-IDAKLTKTSLMRTSNVNGFDFVILEMLVE 425

Qy 408 TVEKPLDHLNALLAGIALPGVNVLLHYVAPEIFVYEGYVWISS 452

Db 426 KIFDLAPNAPNAILGSGVPLKILNIDFSNADIDVLELVLST 470

RESULT 4

LPC3_HUMAN STANDARD; PRT; 477 AA.

AC P59826;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE 10-OCT-2003 (Rel. 42, Last annotation update)

DE Long palate, lung and nasal epithelium carcinoma associated protein 3 precursor (RYA3).

GN LPLUNC3 OR C200R185.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.

RC MEDLINE=22721692; PubMed=12837268;

RA Andraut J.-B., Gaillard I., Giorgi D., Rouquier S.;

RT "Expansion of the BPI family by duplication on human chromosome 20: characterization of the RY gene cluster in 20q11.21 encoding olfactory transporters/antimicrobial-like peptides.,"

RL Genomics 82:172-184(2003).

[2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Sabbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.J., Howden P.J., Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Leharlaib M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lawlor J.E., Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wali M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilting L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;

RT "The DNA sequence and comparative analysis of human chromosome 20.,"

RL Nature 414:865-871(2001).

RN [3]

RP TISSUE SPECIFICITY.

RX MEDLINE=21968577; PubMed=11971875;

RA Bingle C.D., Craven C.J.;

RT "PLUNC: A novel family of candidate host defence proteins expressed in the upper airways and nasopharynx.,"

RL Hum. Mol. Genet. 11:937-943(2002).

CC -!- FUNCTION: May have the capacity of recognizing and binding specific classes of odorants, may act as carrier molecules, transporting odorants across the mucus layer to access the receptor sites. May serve as a primary defense mechanism by recognizing and removing potentially harmful odorants or pathogenic microorganisms from the mucosa or clearing the excess odorant from the mucus to enable new odorant stimuli to be received (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity). Cytoplasmic according to Ref.1.

CC -!- TISSUE SPECIFICITY: Detected in nasal septal epithelium.

CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP family.

CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.

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CC -----

DR EMBL; AF549189; AAP84989.1; .

DR EMBL; AL121756; CAC18886.1; ALT_SEQ.

DR Genbank; HGNC:16178; C20orf185.

DR InterPro; IPR001124; LBP_BPI_CETP.

DR Pfam; PF02886; LBP_BPI_CETP_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

DR PROSITE; PS00490; LBP_BPI_CETP; FALSE_NEG.

DR SIGNAL.

KW CHAIN 1 20 POTENTIAL.

FT 21 477 LONG PALATE, LUNG AND NASAL EPITHELIUM

FT DOMAIN 17 233 CARCINOMA ASSOCIATED PROTEIN 3.

FT CARBOHYD 143 143 LEU/GY-RICH.

FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 17 17 MISSING (IN REF.1).

SQ SEQUENCE 477 AA; 50505 MW; 00C83FDF468BB9F6 CRC64;

Query Match 17.0%; Score 386; DB 1; Length 477;

Best Local Similarity 28.3%; Pred. No. 2.9e-20;

Matches 136; Conservative 90; Mismatches 207; Indels 48; Gaps 13;

QY 9 LVAL--LPLVVGASTP-----GTVRLNKAALSYV---SEIGKAPLQAL-QVT- 52

Db 4 VMLALWSLLMLGLATPYCOELLETVGLTARIDKDELGAIQNSLVGEPIQLVGLSVTA 63

QY 53 VPHEFDWSGEAL-----OPIRILNVHVRHLKFIAGGVRLAAAN 96

Db 64 VNRGLSGGLIGGGGLLGHGGVGVVEELSGUKHEELTPKVLKLLPFGVQL----S 119

QY 97 FTFKV-FRAPEP-----LELTPELLADTRVTQSSIRTPVWSISACSLFSGHANEDGSN 151

Db 120 LHTKVGHCSPGLGILLQLAAEAVNTSRVALAVSSRGTFILILKRCSTLGLHSLFSGLL 179

QY 152 STSHALLVLVQKHIAVLSNKLCLISNLVQGVNVHLGILGNVPGPSQIRYSMVSV 211

Db 180 PT--FLFGVVEQMLPKVLPGLLCPVVDVSVLGVNELLGAVLGLVSLGALGSVEFSLATLP 237

QY 212 TVTSDYISLVNNAVL--ELLGKPIILPTDTPVLRHVTGEGSMATVGLSQOLFDSALL 270

Db 238 LISNQYIELDINPIKSVAGNDIIDFPKRAPAKVP---PKDHTSQVMVPLYLENTFGL 294

271 LKAGALNLDITQRLSDNLTNSALGRLEFVARQPEPMPVVLKVLGATPWAHLT 330
 295 LQINGALDMDITPELVSDPLATTDLAALFPAALGKPLHQLQLLELRVREAPTTLHN 354
 331 NNATLRLQPEVEVLATASAFSLSDVVMRLQLSVKVLQGTTSVLGDVQLTVA 390
 355 KQALVSLPANIHLFFVYKGTPELSPFNLSWTVRAQLAPSAKHLHLSL-LERLSVKVA 413
 391 SSMVGFIDTQVETLMTGTFEKLPHDLHALLAMGLALPGVNLHYVAPFIFYEGYVVI 450
 414 SSTHAFDGRLEBWLSHVGVAYAPKLVNVALDVGILPKVGNFNSVLEIVENAVL 473
 451 S 451
 474 T 474

RESULT 5
 LPC3_MOUSE STANDARD; PRT; 472 AA.
 AC Q80ZU7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Long palate, lung and nasal epithelium carcinoma associated protein 3
 GN LPLUNC3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares V.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton B., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.X.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).

!- FUNCTION: May have the capacity of recognizing and binding
 specific classes of odorants, may act as carrier molecules,
 transporting odorants across the mucus layer to access the
 receptor sites. May serve as a primary defense mechanism by
 recognizing and removing potentially harmful odorants or
 pathogenic microorganisms from the mucosa or clearing the excess
 odorant from the mucus to enable new odorant stimuli to be
 received (By similarity).

!- SUBCELLULAR LOCATION: Secreted (By similarity).
 !- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
 family.

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or send an email to license@isb-sib.ch.
 CC EMBL; BC048084; AAH48084.1; -
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
 DR SMART; SM00328; BPT1; 1.
 DR SMART; SM00329; BPT2; 1.
 DR PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
 KM SIGNAL.
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 20 472 LONG PALATE, LUNG AND NASAL EPITHELIUM
 FT CARBOHYD 20 233 CARCINOMA ASSOCIATED PROTEIN 3.
 FT LEU/GLY-RICH.
 FT CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 472 AA; E80E78B8BD4876 CRC64;
 Query Match 16.8%; Score 380; DB 1; Length 472;
 Best Local Similarity 26.3%; Pred. No. 7.6e-20;
 Matches 126; Conservative 91; Mismatches 208; Indels 54; Gaps 13;
 QY 9 LLLALLPVVG-ASTPTGTVRLNKAALSYVSEIGKA-----PLQALQVTVPH--- 55
 DB 9 LMGLATPCIGLETTVGTTLARIDK-----DELKAIQNSLVGGPILQNLVLTSTVSNQG 62
 QY 56 -----FLDKSG-----EALQPTIRILNVHVRHLKFIAGFGVRLAAANFT 98
 DB 63 LLGAGSLGGGLLSYGGIFSLVEELSGLKISELT--LPKVSULKLPVGVGVL---NLH 116
 QY 99 EKV-FRAPEP---LELTLPVELLADTRVTQSSIRTPVVSISACLSFSGHANEDGSNST 153
 DB 117 TKVSLHGSGPLVGLLQALAEVNVSSVALGMSPRGTPIFLVKRCSTLGLHLSMGLLPT 176
 QY 154 SHALLVVLQKHIAVLSNKLCLISNLVQGVNHLGTLGLNLPVGPSPQIRYSMVSVTV 213
 DB 177 --PIFLGVEQLCKVLPGLCPVVDVSVLWNEELGATLSLPLGLPGVSEFTTLATPLI 234
 QY 214 TSDYISLEVNVL-FLIGKPEIILPTDTPVLPVLRHVGTGSMATVGLSQQLFDSALLLIQ 272
 DB 235 SNQYIELDINPIKYSIAGOVIDFKPIPKVP2---PKEDHTSQVTVPLVLFSTVFGLLQ 291
 QY 273 KAGALMDITQRLSDNLTNSALGRLEFVARQPEPMPVVLKVLGATPWAHLTNN 332
 DB 292 TNGALDLDITPEVPRNVPLTTDLAALAPALGKLPAPQAHLHLSLRVTKSPVLLQNKX 351
 QY 333 ATLRLOPFVEVLATASAFSLSDVVMRLQLSVKVLQGTTSVLGDVQLTVA 392
 DB 352 ATVSIPVTHVLSVSSVPGTPEVAFQNLGNGVNTNAHLAPSTKHLHLSL-LERLSVQLASS 410
 QY 393 NVGFIDTQVETLMTGTFEKLPHDLHALLAMGLALPGVNLHYVAPFIFYEGYVVI 451
 DB 411 FPQPFASRLSEWLSVWVRAAYMQRNLNEHLEVGILPKLVNPNFANSVVDIENAVLIT 469

RESULT 6

LPC4_HUMAN

ID LPC4_HUMAN

AC P59827;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Long palate, lung and nasal epithelium carcinoma associated protein 4

DE (RY2G5).

GN LPLUNC4 OR C20ORF186.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.

RC TISSUE=Fetal brain;

RX MEDLINE=22721692; PubMed=12837268;

RA Andraut J.-B., Gaillard I., Giorgi D., Rouquier S.;

RT "Expansion of the BPI family by duplication on human chromosome 20:

RT Characterization of the RY gene cluster in 20q11.21 encoding olfactory
 RL transporters/antimicrobial-like peptides.";
 RN Genomics 82:172-184 (2003).

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;
 RA Delcukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguale C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck J., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharshaiho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Rosa M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RA "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:863-871 (2001).

CC -!- FUNCTION: May have the capacity of recognizing and binding
 CC specific classes of odorants, may act as carrier molecules,
 CC transporting odorants across the mucus layer to access the
 CC receptor sites. May serve as a primary defense mechanism by
 CC recognizing and removing potentially harmful odorants or
 CC pathogenic microorganisms from the mucosa or clearing the excess
 CC odorant from the mucus to enable new odorant stimuli to be
 CC received (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
 CC family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF549190; AAP84990.1; -

CC EMBL; AL121756; CAC18887.1; -

CC Genew; HGNC:16179; C20orf186.

CC InterPro; IPR001124; LBP_BPI_CETP.

CC Pfam; PF02886; LBP_BPI_CETP_C; 1.

CC SMART; SM00328; BPI2; 1.

CC SMART; SM00329; BPI2; 1.

CC DOMAIN 92 187

CC SEQUENCE 575 AA; 60950 MW; D4B804F446EF7707 CRC64;

CC GLY-RICH.

Query Match 15.8%; Score 358; DB 1; Length 575;

Best Local Similarity 25.9%; Pred. No. 3.6e-18;

Matches 105; Conservative 81; Mismatches 185; Indels 34; Gaps 6;

QY 67 TRIRLVVRLHLKFTAGFCVGRLLAARNTFKVRAPEPELETLPEVLLADTVTQSS 126

DB 186 TGLRIVELTLPRVSLRPLPGVGVLSLRYVAINGSKSLGFLDIAYEVNITAKVLTWDR 245

QY 127 IRTPVVSVSACSLFSGH-----ANEFGSNTSHALLVLCVCKHKAVLSNKLCLS 176

DB 246 TGYPRLVIERCDTLGGIKVKLLRGLLPNLVDN-----LVNRVYADVLPDLCP 295

QY 177 ISNVLGVNVLHGLTGLGNPVGVPESQIRSVSMVSVPTVTDYISLEVNVL-----F 227

DB 296 VDVVLGVNDQLGVDSLIPLGLIGSVQVTFSSLPVLTGTFLELDLNTLVGEAGGLIDY 355

QY 228 LIGKPIILPTDPTFVLPVPHVGTGSMATVGLSQQLFDSALLLLOKAGALNLDITQOLRS 287

DB 356 PLGWPAVSP-KMPELPMPMDNKTSLA---NSANFLGSLVTLLOKHALELDITNGMPE 411

QY 288 DNNLNTSALGRLEIPEVARQFPEPVPVVLKVRIGATPVAMLHTNATLRLOPPEVLATA 347

DB 412 ELPPIITATGALIEPKVFOQYXPCSLIIRIQVLPNPSVLMQDKALVKVLATAEYVWSQ 471

QY 348 SNSAFQSLFSLDVMNLRQLQSVKVKLQGTTSVLGDVQLTVASSNVGFTDITDQVRLMG 407

DB 472 PKDLTETICLDIVDTFELASFTEGDKLM-IDAKLEKTSINLRSTNSVGNFIDGLMEVIVE 530

QY 408 TVPEKPLDLHALLAMGIALPGVNVHLVVAPEIFVVEGYVVISS 452

DB 531 KTFD-LAFWPAFMANAVLGSVPLFKILNIDFSNADIDVLEDLVLSA 575

RESULT 7

LPC3_RAT

ID LPC3_RAT STANDARD; PRT; 473 AA.

AC Q05701;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Long palate, lung and nasal epithelium carcinoma associated protein 3

DE precursor (potential ligand-binding protein RY43).

GN LPLUNC3 OR RY43.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Fischer; TISSUE=Olfactory epithelium;

RX MEDLINE=92007724; PubMed=1915264;

RA Dear T.N., Boehm T., Keverne E.B., Rabbitts T.H.;

RT "Novel genes for potential ligand-binding proteins in subregions of

RL the olfactory mucosa.";

RL EMBO J. 10:2813-2819 (1991).

CC -!- FUNCTION: May have the capacity of recognizing and binding

CC specific classes of odorants, may act as carrier molecules,

CC transporting odorants across the mucus layer to access the

CC receptor sites. May serve as a primary defense mechanism by

CC recognizing and removing potentially harmful odorants or

CC pathogenic microorganisms from the mucosa or clearing the excess

CC odorant from the mucus to enable new odorant stimuli to be

CC received.

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- TISSUE SPECIFICITY: Highly expressed in olfactory mucosa but

CC undetectable in thymus, kidney, lung, brain, spleen and liver.

CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP

CC family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; X60458; CAA43065.1; -

CC InterPro; IPR001124; LBP_BPI_CETP.

CC Pfam; PF02886; LBP_BPI_CETP_C; 1.

CC SMART; SM00328; BPI1; 1.

CC SMART; SM00329; BPI2; 1.

CC PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.

RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA	Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA	Dami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA	Gilbert J.G.R., Goward M.E., Grafton D.V., Griffiths M.N.D., Hall C.,
RA	Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA	Mccloy J., McLaren S., Mccurray A.A., Milne S.A., Mortimore B.J.,
RA	Ocdell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA	Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA	Vaundon M., Walli M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA	Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA	Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA	Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA	Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA	Lewis J., Lewis S., Lin S.-P., Loh P., Malaaj E., Nguyen T., Pan H.,
RA	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA	Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA	Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA	Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA	Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA	Hinds K., Kemp K., Latrelle P., Layman D., Ozersky P., Rohlfing T.,
RA	Schneet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA	Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA	Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA	Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA	Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA	Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA	O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA	Khan A.S., Lane L., Tiliakou Y., Wright H.;
RT	"The DNA sequence of human chromosome 22.";
RL	Nature 402:489-495(1999).
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC	-1- TISSUE SPECIFICITY: Detected in the basal layer of the epidermis
CC	from inflammatory skin from psoriasis patients, but not in normal
CC	skin.
CC	-1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC	family.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF465766; AAM73984.1; -;
DR	EMBL; AL021937; -; NOT ANNOTATED_CDS.
DR	Genew; HGNC:16503; BPII2
DR	InterPro; IPR001124; LBP_BPI_CETP.
DR	Pfam; PF01273; LBP_BPI_CETP; 1.
DR	Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR	SMART; SM00328; BPII; 1.
DR	SMART; SM00329; BPI2; 1.
DR	PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
KW	Signal.
FT	SIGNAL. 1 23 POTENTIAL.
FT	CHAIN 24 507 BACTERICIDAL/PERMEABILITY-INCREASING
FT	PROTEIN-LIKE 2.
FT	CARBOHYD 79 79 N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD 92 92 N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD 113 113 N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD 213 213 N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD 225 225 N-LINKED (GLCNAC. -) (POTENTIAL).

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FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 507 AA; 56469 MW; C45285C62SAC08E2 CRC64;

Query Match
Best Local Similarity 14.6%; Score 330.5; DB 1; Length 507;
Matches 117; Conservative 96; Mismatches 231; Indels 33; Gaps 12;

QY 8 GLLALLPVGAST--PGTVRLNKAALSYSEIGKAPLQAL-QVTVPHEFDWSG-EA 63
Db 11 GCLLNLNLYSSQTTIPGKARITQALDYGVQAGMKVTEQMLKPKLP---DLSCSES 67
QY 64 LQPTRIRILNVH-----VRLHLKFIAGEGVRL--AAAN-----FTFKVFA 104
Db 68 LFLKVDYVYNFNSNIKISAFSEPTSLAFVPGVGHKALNTHGTANLSTWDGSESLFQD 127
QY 105 PBPLETLP-VELLADTRVTOSSIRTPVVSISACSLFSGHAN-EFDGNSNTH-ALLVLV 161
Db 128 TGSADLFLSGVFTGIIITLREDFGHPTLKIQCYAQLSHARVFSSELVLVNSFAEPM 187
QY 162 QKHIVKLVNKLCLSLNVOGVNVEGLTGLNLPVGPESQIRYMSVPTVTSVISIE 221
Db 186 EXPILKLNLEMLCPPIASEVKALNANLSTLEVTIKIDNTYLLDYS--SSPEITENYLDN 247
QY 222 VNVLFLGKPIILPTDTPFVLRHVGTGEGMATVGLSQQLFDSALLLQKAGALNDI 281
Db 248 LKGVFYLENLTDPPSPVPVFLPER---SNKLYIGIAEYFKSAFAHFTAGVFNVL 304
QY 282 TQLRSDNLLNTSLGRILPEVARQFPEPMPVLKVRLGATVPVAMLTNNATRLQPFV 341
Db 305 STEEISNHFVQSGGLNVLRIAEIYLSQPFVVRIMATEPPIINLQPGNFTLDPASI 364
QY 342 EVLATASNAFQSLSDVWNLRLQLSVKVQLQTTISVLGDVQLTVASSNVGFDITQ 401
Db 365 MMLTPQKSTVETIVSMDFVASTVSGVLQILQVLCSL-LNRFRLALPESNRNIEVL 423
QY 402 VRLMGTVFEKPLDHLNALLAMGIALPGVNLHLYVAEIVFVGVVTSGLFYQS 458
Db 424 FENILSSILHFGVLPANAKLQGGFPLSNPKFLFVNSDIEVLESELLISTDLKYE 480

RESULT 9
BPL2 MOUSE
ID BPL2 MOUSE STANDARD; PRT; 509 AA.
AC Q8C186;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bactericidal/permeability-increasing protein-like 2 precursor.
GN BPL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

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RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana A., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kichikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.
KL Nature 420:563-573 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC
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CC
CC -----
CC EMBL; AK028764; BAC26108.1; -
CC InterPro; IPR001124; LBP BPI CFTP.
CC Pfam; PF01273; LBP BPI CFTP; 1.
CC SMART; SM00328; BPI1; 1.
CC SMART; SM00329; BPI2; 1.
CC PROSITE; PS00400; LBP_BPI_CFTP; FALSE_NEG.
CC SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT BACTERICIDAL/PERMEABILITY-INCREASING
FT PROTEIN-LIKE 2.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 509 AA; 56616 MW; 07A1E2DBAA24BD9A CRC64;

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Query Match 13.8%; Score 313.5; DB 1; Length 509;
Best Local Similarity 23.4%; Pred. No. 4.7e-15;
Matches 112; Conservative 98; Mismatches 231; Indels 37; Gaps 13;

QY 9 LLLALLPVGASTPGTVRLNKAALSYSEIGKAPL-QRALQVTPHFDWSG-EALQP 66
Db 14 LLWSLYASSQTVTGTARITQALDYGLQVGMKVLQAKLIVP---DLNGSESLKF 70
QY 67 TRI-----RIILNVH-----PRLHLKFIAGEGVRLA-----AANFTK--VERAPEP 107
Db 71 LKIDVYKYNFNSKINAFSPNTSLAFVPGVGHKALNTHGTANLSTWDGSESLFQD 130
QY 108 LELTLP-VELLADTRVTOSSIRTPVVSISACSLFSGHAN-EFDGNS--NSTSHALLVL 160
Db 131 ANLFLSGIYFTGIVAFTRNDFGYPALQLQDCHVQSHARVFSSELVLVNSFAEPMK 190
QY 161 VOXHIKVLNKLCLSLNVOGVNVEGLTGLNLPVGPESQIRYMSVPTVTSVISIE 220
Db 191 ILKMLNEMW--QLCPIALSQVEQFNVALEVTUKIDNTYLLDYS--SSPEITENYLD 248
QY 221 EVNAVLF-LGKPIILPTDTPFVLRHVGTGEGMATVGLSQQLFDSALLLQKAGALND 280

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OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-64.
 RX MEDLINE=89255455; PubMed=2722846;
 RA Gray P.W., Flagg G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,
 RA Elsbach P.;
 RT "Cloning of the cDNA of a human neutrophil bactericidal protein.
 RT Structural and functional correlations.";
 RL J. Biol. Chem. 264:9505-9509(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94292492; PubMed=7517398;
 RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
 RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
 RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
 (LPS)-binding protein. LPS binding properties and effects on LPS-
 mediated cell activation.";
 RL J. Biol. Chem. 269:17411-17416(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Xu J., Wang H.;
 RA "Cloning of cDNA of human bactericidal/permeability-increasing
 RT protein.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaevaiaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitbread S.J., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [5]
 RP SEQUENCE OF 28-42.
 RX MEDLINE=88333057; PubMed=3667613;
 RA Ooi C.E., Weiss J., Elsbach P., Frangione B., Mannion B.;
 RT "A 25-kDa NH2-terminal fragment carries all the antibacterial
 RT activities of the human neutrophil 60-kDa
 RT bactericidal/permeability-increasing protein.";
 RL J. Biol. Chem. 262:14891-14894(1987).
 RN [6]
 RP SEQUENCE OF 28-47.
 RX MEDLINE=89315847; PubMed=2501794;
 RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
 RA Marra M.N., Seeger M., Nathan C.F.;
 RT "Antibiotic proteins of human polymorphonuclear leukocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=97334442; PubMed=9188532;
 RA Beamer L.O., Carroll S.F., Eisenberg D.;

RT "Crystal structure of human BPI and two bound phospholipids at 2.4-A
 RL resolution.";
 RL Science 276:1861-1864(1997).
 CC -!- FUNCTION: The cytotoxic action of BPI is limited to many species
 CC of Gram-negative bacteria; this specificity may be explained by a
 CC strong affinity of the very basic N-terminal half for the
 CC negatively charged lipopolysaccharides that are unique to the
 CC Gram-negative bacterial outer envelope.
 CC SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED IN POLYMORPHONUCLEAR
 CC LEUKOCYTES (PMN) GRANULES.
 CC -!- TISSUE SPECIFICITY: Restricted to cells of the myeloid series.
 CC -!- DOMAIN: The N-terminal region may be exposed to the interior of
 CC the granule, whereas the C-terminal portion may be embedded in the
 CC membrane. During phagocytosis and degradation, proteases may be
 CC released and activated and cleave BPI at the junction of the N-
 CC and C-terminal portions of the molecule, providing controlled
 CC release of the N-terminal antibacterial fragment when bacteria are
 CC ingested.
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
 CC family.
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 DR EMBL; J04739; AAA51841.1; ALT INIT.
 DR EMBL; AF322588; AAG42844.1; -;
 DR EMBL; AL359555; CAC13043.1; -;
 DR EMBL; AL499625; CAC27350.1; -;
 DR EMBL; AL391692; CAC10453.1; -;
 DR PDB; 1BP1; 04-SEP-97.
 DR PDB; 1BWF; 21-JUN-00.
 DR Genew; HGNC:1095; BPI.
 DR MIM; 109195; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR InterPro; IPR001124; LBP BPI CTFP.
 DR Pfam; PF01273; LBP_BPI_CTFP_1.
 DR Pfam; PF02886; LBP_BPI_CTFP_C; 1.
 DR SMART; SM00328; BPI1; 1.
 DR SMART; SM00329; BPI2; 1.
 DR PROSITE; PS00400; LBP BPI CTFP; 1.
 KW Antibiotic; Signal; Transmembrane; Glycoprotein; 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 483 BACTERICIDAL PERMEABILITY-INCREASING
 FT PROTEIN.
 FT SITE 236 241 CLEAVAGE SITES FOR ELASTASE (POTENTIAL).
 FT TRANSMEM 365 385 POTENTIAL.
 FT CONFLICT 12 12 V -> A (IN REF. 3 AND 4).
 FT CONFLICT 212 212 K -> E (IN REF. 4).
 FT CONFLICT 351 351 P -> S (IN REF. 3).
 FT CONFLICT 371 371 F -> L (IN REF. 2).
 FT CONFLICT 400 400 N -> D (IN REF. 3).
 FT CONFLICT 407 407 K -> R (IN REF. 3).
 FT STRAND 32 37
 FT HELIX 38 56
 FT TURN 57 58
 FT STRAND 64 70
 FT TURN 71 73
 FT STRAND 74 89
 FT STRAND 93 98
 FT TURN 99 101
 FT STRAND 102 122
 FT TURN 123 124
 FT STRAND 125 149
 FT TURN 150 153
 FT STRAND 154 163
 FT STRAND 168 172
 FT TURN 174 175
 FT HELIX 179 188

FT TURN 189 189
 FT HELIX 217 217
 FT TURN 218 218
 FT STRAND 223 225
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 FT STRAND 241 242
 FT STRAND 246 251
 FT STRAND 254 257
 FT STRAND 281 286
 FT STRAND 287 299
 FT TURN 300 301
 FT STRAND 304 307
 FT HELIX 309 311
 FT STRAND 321 321
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 FT TURN 326 328
 FT TURN 330 331
 FT HELIX 332 335
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 FT STRAND 352 356
 FT TURN 357 358
 FT STRAND 359 363
 FT STRAND 365 373
 FT TURN 375 376
 FT STRAND 379 388
 FT STRAND 392 398
 FT TURN 399 400
 FT STRAND 401 408
 FT STRAND 412 412
 FT STRAND 415 418
 FT TURN 419 420
 FT HELIX 425 428
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 FT TURN 458 459
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 FT TURN 471 472
 FT STRAND 473 483
 SQ SEQUENCE 483 AA; 53396 MW; AD58C92BCAD8F47C CRC64;

Query Match
 Best Local Similarity 22.4%; Pred. No. 6.6e-13;
 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLPVGASTPGTVVRKKAALSYVSEIGKAPLQAL-QVTVPFLD--- 58
 DB 11 WVS-LMWLVAGTAVTAAVNPGVWVRSIQKGLDYASQQTALQKELKRIKIPDYSDSEK 69
 QY 59 -----WSGALQPTRIILNVH---VPRHLKF-IAGFGVRLAAANFTKVFRAPE 106
 DB 70 IKHLGKHYSFYSDMIREFQLPSSQISMVYPVGLKFSISNANIKISGRKWAQKRFKMSG 129
 QY 107 PLELTP-VELLADTRV-TQSGIRTPVVSISACSLFSGHANEFDGNSVSHA--LLVLVQ 162
 DB 130 NFDLSIEGMSIADLXLSNPTSGKPTTCSC---SSHINSVHVHISKVGWLLQLEPH 186
 QY 163 KHIAVLNKL----CLSIENLVQ--VNVHLGTLGLNPNVGPESQTRYSMVSVPTTSY 217
 DB 187 KKIESALRNKMSQCEKVTNSVSSKLPQFYQTLFPMTKIDSVAG-NYGLVAPPATTAT 246
 QY 218 ISLEVNVLFLGKPIILPTDTPVLP--RHVGTEGSMATVGLSQCLPDSALLLQKAG 275
 DB 247 LDVQMGKEFYSENH-----HNPPFPAPPVMEFPAADRMVVLGSLFYFNTAGLVQEAG 301
 QY 276 ALNLDTGL--RSDNLLNTSALGRLIPEVARQPEPVPVLKRLGATPVAKLHTNNA 333
 DB 302 VLKTLRDMIPKESKRLTKFQTEFLPEVAKKFPN---MKIQIHVSASTPPLSVQPT 358
 QY 334 TLRLOPFVEVLATA--SNSAFOSLFLSDVNNLRQLSKVSKVLOQTTSVLGDVCLTVAS 391
 DB 359 GLTFEPAVDVQAFVLPNSLSLASLFLIGHMTTGSMEVSAESNRLVGELK-LDRLLLELKH 417

QY 392 SNVGFIDTDQVRLTGMVTFEKLPLDLHLLALLANGIALPGVNNLHVVAPEIFVYEGVVIS 451
 DB 418 SNIGPFPVELLDIMNVIPIVLPRVNEKQKGFPLETPARVQLYNNVQLPHQNFLEEG 477
 QY 452 SGLFYQ 457
 DB 478 ADVVIK 483
 RESULT 12
 BPL3_MOUSE
 ID_BPL3_MOUSE STANDARD; PRT; 449 AA.
 AC Q8BU51; Q80ZU8;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Bactericidal/permeability-increasing protein-like 3 precursor.
 GN BPLI3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA *Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 335-449 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Shirazee-Kishikawa T., Kohno H., Makamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,


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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).  
CC -!- SIMILARITY: Belongs to the BPI/LBP/plunc superfamily. BPI/LBP  
family.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: AK087711; BAC39978.1; ALT INIT.  
CC EXBL: BC048083; AAH48083.1; -.  
CC InterPro: IPR001124; LBP_BPI_CETP.  
CC SMART: SM00329; BPI2; 1.  
CC PROSITE: PS00400; LBP_BPI_CETP, FALSE_NEG.  
KW Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 449 BACTERICIDAL/PERMEABILITY-INCREASING  
FT CHAIN 19 449 PROTEIN-LIKE 3.  
FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 385 386 FP -> SS (IN REF. 2).  
FT SEQUENCE 449 AA; 48901 MW; EF4290C3C8301DD6 CRC64;  
SQ  
Query Match 12.4%; Score 280; DB 1; Length 449;  
Best Local Similarity 23.9%; Pred. No. 9.9e-13;  
Matches 111; Conservative 94; Mismatches 215; Indels 44; Gaps 15;  
Qy 7 LGILLALLPVVGASTCTGTVVRINKAALSYSEIGKAPLQALQVTPHFID-WSGERALQ 65  
Db 5 LSLVLCGLLAGTRAD-PGGLRLRGDINNH-----EVQSAMEES--HILERMAEASN 54  
Qy 66 P-----TRIRLVHVPRLHLKFIAGFVRLAAANFTF--KVFRAPPELELTLP 113  
Db 55 PQGGKAIKGLSNMKKVDLEPVTINFPVGVISQCVSTGWTGKFTGNG-WEINVV 113  
Qy 114 VELLADTRVQ--SRITFVWSISACS--LFSGHANEFGSNTSHALVLVQKHKAVLS 170  
Db 114 LNIATDRLQDEBAG-EVFRSEGEVILSVKTN-----LPNNKAIKFKVDSTLRKVL 168  
Qy 171 NKLCLISNLVQGVNHLGTLGLNPGVCPESQIRYSVMVSVPTVTSDXLSLEFNAVLFL- 229  
Db 169 GLMCPALDANLVEYVNNKKAKLTDMPVDKGTIVKIAUTSPPATFASHIQVDFSPVQLQE 228  
Qy 230 GKPIILPTDTPFVLRHVGTGEGMATVGLSQQLFDSALLLQKAGALNL--DITGQLRS 287  
Db 229 GOLIQLATDGS--LPEFPEGSANDSQLLSATFTLAEALLQKLSLEVLKDKRKGKLPQ 285  
Qy 288 DDNLNLSALGRLLPEVARQPEPMPVVLKVLRLGATGVAMHTNATLRLQFFVEVLATA 347  
Db 286 ----NRTLAFIPQVAKTKPKPLIKVINKPKPVTKMAGKSLMLHLSLEMPFAAR 340  
Qy 348 SNSAF-QSLFSLDVVNLRLQISYKVKLGTSVGLGVQVLTVAASNNGVFDITDQVRLX 406  
Db 341 RHGKPKSLFFLETHIGLEIHYQDNPLQMTSMDSLSLARFPFSQDFHEAELTGF- 400  
Qy 407 GTVPEKPLLDHNLALAMGIALPGVNLVHYVAEIPFVYGVVVI 450  
Db 401 TDY-QKAVIPVNDVHLVGLPLDLLAINYNLAELDIVEDALVL 444  
RESULT 13  
ID_LBP_HUMAN STANDARD; PRT: 481 AA.  
AC P18428; O43438; Q92672; Q9H403; Q9UD66;  
DT 01-NOV-1990 (Rel. 16, Created)
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DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Lipopolysaccharide-binding protein precursor (LBP).  
GN LBP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90385281; PubMed=2402637;  
RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,  
RA Lane J.C., Tobias P.S., Ulevitch R.J.;  
RA "Structure and function of lipopolysaccharide binding protein.";  
RL Science 249:1429-1431 (1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9429492; PubMed=7517198;  
RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,  
RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;  
RA "Bactericidal/permeability-increasing protein and lipopolysaccharide  
RT (LPS)-binding protein. LPS binding properties and effects on LPS-  
RT mediated cell activation.";  
RL J. Biol. Chem. 269:17411-17416 (1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98110577; PubMed=9441745;  
RA Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,  
RA Seilhamer J.J., Schumann R.R.;  
RA "Similar organization of the lipopolysaccharide-binding protein (LBP)  
RT and phospholipid transfer protein (PLTP) genes suggests a common gene  
RT family of lipid-binding proteins.";  
RL Genomics 46:416-425 (1997).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;  
RA "Cloning and sequencing of human lipopolysaccharide-binding protein  
RT gene.";  
RL Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:469-471 (1998).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21638749; PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.B., Corby N.R.,  
RA Cousion A., Coville G.J., Deadman R., Dhami P.D., Dunn X.,  
RA Ellington A.G., Frankland J.A., Fraser A., Frech L., Garner P.,  
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S.C., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";
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RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=97289150; PubMed=9144073;
 RA Lengacher S., Jongeneel C.V., Le Roy D., Lee J.D., Kravchenko V.,
 RA Ulevitch R.J., Glauser M.P., Heumann D.,
 RA "Reactivity of murine and human recombinant LPS-binding protein (LBP)
 RC within LPS and Gram-negative bacteria.";
 RL J. Inflamm. 47:165-172(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Kuzny D.M., Sodergren E.C., Lu X., Gibbs R.A., Scheetz A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds to the lipid A moiety of bacterial
 CC lipopolysaccharides (LPS) a glycolipid present in the outer
 CC membrane of all Gram-negative bacteria. The LBP/LPS complex seems
 CC to interact with the CD14 receptor.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
 CC family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC
 DR EMBL; X99347; CAAG7271.1; -;
 DR EMBL; BC004795; AAH04795.1; -;
 DR HS92; P17213; BPI.
 DR MGD; MGI:1098776; Lbp.
 DR GO; GO:0001530; F:lipopolysaccharide binding; IDA.
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF01273; LBP_BPI_CETP_1.
 DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
 DR SMART; SM00328; BPI1; 1.
 DR SMART; SM00329; BPI2; 1.
 DR PROSITE; PS00400; LBP_BPI_CETP; 1.
 RN Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 481
 FT CARCXYD 300 300
 FT CARCXYD 355 355
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 FT CONFLICT 51 51
 FT CONFLICT 102 102
 FT CONFLICT 122 122
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SQ SEQUENCE 481 AA; 53312 MW; 34EA9C06G9AB678 CRC64;
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 Best Local Similarity 24.7%; Pred. No. 4.4e-11;
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 QY 7 IGLLALLPVVGASTPGTGVRLNKAALSYSEIGKAPLORAL-QVTPHELDWSE--- 62
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 QY 63 -----ALQPTIRILNVHVRHLHLKFTAGVRLAA-----ANFTKVFAPRPLE-- 109
 DB KAVRGQGYEHSLEIQNCELRGSSSLKLLPGQLRLAISDSSIGVGKKVKRKSFLKLHGS 128
 QY 110 -----LTLPEVLLADRVVTQSSIRTPWVSISACSL-----FSGHA-----NEFDGS 150
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 QY 151 NSTSHALLVVKQHKIKAVLSNKLCLSI-SNLVQGVNVHGLTILGNLPVGPESQ----TRY 205
 DB -----IESKLQKVLNKKVCEMIQKSVTSDLQPYLQTL-----PVTAEIDNVLGIDY 230
 QY 206 SMVSVPTVTSYISLEVNNAVLFLLG--KPIILPTDATPFVLPVRHVTGSGMATVGLSOOL 263
 DB SLVAAPQAKAQLVDVNFKEIFNRRHSFVATPTPT--MSLPE---DSKQMYFAISDHA 285
 QY 264 FDSALLLQKAGALNDITGQLRSDDN--LNTSALGRLLPEVARQFPPEPMEVVLKVRIG 321
 DB FNIASRVVHQAGYLNFSITDDMLPHDSGIRLNTKAFRPTPIQYKKYPDMKLELLRTVVS 345
 QY 322 ATFEVAMLTNNATLRLQPFVEVLATASNASQSLFSLDVVNNLRLOLSVKVKLOGTTISV 381
 DB A-FILNVPGNLSLAPQMEIEGFVILPTSAPEVFLSVTVNVFASLTNTKRTKVTGMLHP 404
 QY 382 LGDVQLTWASSNVGFIIDQVETLGMGTVEKPELDELHALLAMG--IALPGVVNHLHYAP 439
 DB -DKAQVRLESKVGIFNVNLFQAFNLNYLLNSLYPDVNAELAQGPFLPLPRHQLHDLDF 463
 QY 440 EI---FVYEG 446
 DB 464 QIRKDFLYIG 473
 RESULT 15
 LBP_RABIT
 ID LBP_RABIT STANDARD; PRT; 482 AA.
 AC P17454;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipopolysaccharide-binding protein precursor (LBP).
 GN LBP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90385281; PubMed=2402637;
 RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,
 RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
 RT "Structure and function of lipopolysaccharide binding protein.";
 RL Science 249:1429-1431(1990).
 RN [2]
 RP SEQUENCE OF 27-66.
 RC TISSUE-Serum;
 RX MEDLINE=86306528; PubMed=2427635;
 RA Tobias P.S., Soldau K., Ulevitch R.J.;
 RT "Isolation of a lipopolysaccharide-binding acute phase reactant from
 RT rabbit serum.";
 RL J. Exp. Med. 164:777-793(1986).
 CC -!- FUNCTION: Binds to the lipid A moiety of bacterial
 CC lipopolysaccharides (LPS), a glycolipid present in the outer

